

FORM PTO-1390  
(REV 10-95)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1781

U.S. APPLICATION NO. (If known, see 37 CFR §1.5)

**09/673840**

INTERNATIONAL APPLICATION NO.

INTERNATIONAL FILING DATE

PCT/DE99/01163

15 April 1999

PRIORITY DATE CLAIMED

21 April 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BLADDER TISSUE

APPLICANT(S) FOR DO/EO/US

SPECHT, Thomas, et al.

**Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:**

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
  2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
  3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
  4. ☐ A proper Demand for International Preliminary Examination was made by the 19<sup>th</sup> month from the earliest claimed priority date.
  5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
    - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
    - b. ☒ has been transmitted by the International Bureau.
    - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
  6. ☐ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
  7. ☐ A copy of the International Search Report (PCT/ISA/210).
  8. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
    - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
    - b. ☐ have been transmitted by the International Bureau.
    - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
    - d. ☒ have not been made and will not be made.
  9. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
  10. ☐ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
  11. ☐ A copy of the International Preliminary Examination Report (PCT/IPEA/409).
  12. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).
- Items 13. to 19. below concern document(s) or information included:**
13. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
  14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included
  15. ☐ A FIRST preliminary amendment.
    - ☐ A SECOND or SUBSEQUENT preliminary amendment.
  16. ☐ A substitute specification.
  17. ☐ A change of power of attorney and/or address letter.
  18. ☐ Certificate of Mailing by Express Mail
  19. ☒ Other items or information:

Sequence Listing with disk

COPY

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| U.S. APPLICATION NO. <b>09/673840</b><br>INTERNATIONAL APPLICATION NO.<br>PCT/DE99/01163 | ATTORNEY'S DOCKET NUMBER<br>SCH 1781 |
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| 17. <input checked="" type="checkbox"/> The following fees are submitted:<br><b>BASIC NATIONAL FEE (37 CFR §1.492 (a) (1) - (5)):</b><br>Search Report has been prepared by the EPO or JPO..... \$860.00<br>International preliminary examination fee paid to USPTO (37 CFR §1.482)..... \$690.00<br>No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$710.00<br>Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO..... \$1,000.00<br>International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$100.00<br><br><div style="text-align: right;"><b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b></div> <div style="text-align: right;">\$860.00</div><br>Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30<br><div style="text-align: right;">\$0.00</div><br><table border="1" style="width:100%; border-collapse: collapse;"> <tr> <th style="width:20%;">CLAIMS</th> <th style="width:20%;">NUMBER FILED</th> <th style="width:20%;">NUMBER EXTRA</th> <th style="width:20%;">RATE</th> <th style="width:20%;"></th> </tr> <tr> <td>Total claims</td> <td>- 20 =</td> <td>0</td> <td>x \$ 18.00</td> <td>\$0.00</td> </tr> <tr> <td>Independent claims</td> <td>- 3 =</td> <td>0</td> <td>x \$ 80.00</td> <td>\$0.00</td> </tr> <tr> <td colspan="4">MULTIPLE DEPENDENT CLAIM(S) (if applicable)</td> <td>+ \$ 270.00</td> </tr> </table> <div style="text-align: right;"><b>TOTAL OF ABOVE CALCULATIONS =</b></div> <div style="text-align: right;">\$860.00</div><br>Reduction of 1/2 for filing by small entity, if applicable. A Verified Small Entity Statement must be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).<br><div style="text-align: right;"><b>SUBTOTAL =</b></div> <div style="text-align: right;">\$0.00</div><br>Processing fee of \$130.00 for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30<br><div style="text-align: right;"><b>TOTAL NATIONAL FEE =</b></div> <div style="text-align: right;">\$860.00</div><br>Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.<br><div style="text-align: right;"><b>TOTAL FEES ENCLOSED =</b></div> <div style="text-align: right;">\$860.00</div><br><table border="1" style="width:100%; border-collapse: collapse;"> <tr> <td style="width:60%;"></td> <td style="width:40%;">Amount to be refunded:</td> </tr> <tr> <td></td> <td>charged:</td> </tr> </table> | CLAIMS                 | NUMBER FILED | NUMBER EXTRA | RATE        |  | Total claims | - 20 = | 0 | x \$ 18.00 | \$0.00 | Independent claims | - 3 = | 0 | x \$ 80.00 | \$0.00 | MULTIPLE DEPENDENT CLAIM(S) (if applicable) |  |  |  | + \$ 270.00 |  | Amount to be refunded: |  | charged: |  |
|---|------------------------|--------------|--------------|-------------|--|--------------|--------|---|------------|--------|--------------------|-------|---|------------|--------|---|--|--|--|-------------|--|------------------------|--|----------|--|
| CLAIMS  | NUMBER FILED           | NUMBER EXTRA | RATE         |             |  |              |        |   |            |        |                    |       |   |            |        |   |  |  |  |             |  |                        |  |          |  |
| Total claims  | - 20 =                 | 0            | x \$ 18.00   | \$0.00      |  |              |        |   |            |        |                    |       |   |            |        |   |  |  |  |             |  |                        |  |          |  |
| Independent claims  | - 3 =                  | 0            | x \$ 80.00   | \$0.00      |  |              |        |   |            |        |                    |       |   |            |        |   |  |  |  |             |  |                        |  |          |  |
| MULTIPLE DEPENDENT CLAIM(S) (if applicable)   |                        |              |              | + \$ 270.00 |  |              |        |   |            |        |                    |       |   |            |        |   |  |  |  |             |  |                        |  |          |  |
|   | Amount to be refunded: |              |              |             |  |              |        |   |            |        |                    |       |   |            |        |   |  |  |  |             |  |                        |  |          |  |
|   | charged:               |              |              |             |  |              |        |   |            |        |                    |       |   |            |        |   |  |  |  |             |  |                        |  |          |  |

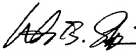
  

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| a <input checked="" type="checkbox"/> A check in the amount of <u>\$860.00</u> to cover the above fees is enclosed.<br><br>b <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$_____ to cover the above fees. A duplicate copy of this sheet is enclosed.<br><br>c <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed. |  |
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**NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.**

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| SEND ALL CORRESPONDENCE TO<br>MILLEN, WHITE, ZELANO & BRANIGAN, P.C.<br>Arlington Courthouse Plaza I<br>2200 Clarendon Boulevard, Suite 1400<br>Arlington, Virginia 22201<br>(703) 243-6333 | <div style="text-align: center;"> <br/>         SIGNATURE<br/> <hr/>         Harry B. Shubin<br/>         NAME<br/> <hr/>         32,004<br/>         REGISTRATION NUMBER       </div> |
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Filed: October 23, 2000

AJZ(HBS): jmm k:\pat\sch\1781\natl phase transmtl

RECEIVED 6 MAR 2001

IN THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

International Application No. : PCT/DE99/01163  
International Filing Date : 15 APRIL 1999  
U.S. Serial No. : 09/673,840  
Deposit Date U.S. Nat'l Phase : 23 OCTOBER 2000  
Priority Date(s) Claimed : 21 APRIL 1998  
Applicant(s) : SPECHT, Thomas, et al.  
Title: HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE

PRELIMINARY AMENDMENT

Commissioner for Patents  
Box PCT  
Washington, D.C. 20231

Sir:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

IN THE CLAIMS:

3. (Amended) Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2, characterized in that they are expressed elevated in normal bladder tissue.
4. (Amended) BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for use as vehicles for gene transfer.
5. (Amended) A nucleic acid sequence according to claim 1, wherein it has 90% homology to a human nucleic acid sequence.
6. (Amended) A nucleic acid sequence according to claim 1, wherein it has 95% homology to a human nucleic acid sequence.
7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claim 1, in such a sufficient amount that they hybridize with the sequences according to claim 1.

8. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. (Amended) A nucleic acid sequence according to claim 1, which codes at least one partial sequence of a bioactive polypeptide.

11. (Amended) An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 1, together with at least one control or regulatory sequence.

13. (Amended) An expression cassette according to claim 11, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. (Amended) Use of nucleic acid sequences according to claim 1 for producing full-length genes.

16. (Amended) Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to claim 1.

18. (Amended) Host cell according to claim 16, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. (Amended) A process for producing a polypeptide or a fragment, wherein the host cells according to claim 16 are cultivated.

27. (Amended) Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as tools for finding active ingredients against the bladder tumor.

28. (Amended) Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. (Amended) Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 in sense or antisense form.

30. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 for the production of a pharmaceutical agent for treatment of the bladder tumor.



32. (Amended) Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431 of claim 23.

33. (Amended) A nucleic acid sequence according to claim 1, wherein it is a genomic sequence.

34. (Amended) A nucleic acid sequence according to claim 1, wherein it is an mRNA sequence.

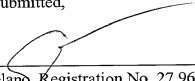
35. (Amended) Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403 of claim 2.

38. (Amended) A nucleic acid sequence according to claim 1, wherein the size of the fragment has a length of at least 300 to 3500 bp.

#### REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Respectfully submitted,



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Filed: 6 MARCH 2001

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Claims 3-11, 13-14, 16, 18-19, 27-35 and 38 have been amended as follows:

3. (Amended) Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2, characterized in that they are expressed elevated in normal bladder tissue.

4. (Amended) BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for use as vehicles for gene transfer.

5. (Amended) A nucleic acid sequence according to ~~claimsclaim~~ 1-~~to 4~~, wherein it has 90% homology to a human nucleic acid sequence.

6. (Amended) A nucleic acid sequence according to ~~claimsclaim~~ 1-~~to 4~~, wherein it has %~~95~~ homology to a human nucleic acid sequence.

7. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in ~~claimsclaim~~ 1-~~to 6~~, in such a sufficient amount that they hybridize with the sequences according to ~~claimsclaim~~ 1-~~to 6~~.

8. (Amended) A nucleic acid sequence according to ~~claimsclaim~~ 1-~~to 7~~, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. (Amended) A nucleic acid sequence according to ~~claimsclaim~~ 1-~~to 7~~, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. (Amended) A nucleic acid sequence according to ~~one of claimsclaim~~ 1-~~to 9~~, which codes at least one partial sequence of a bioactive polypeptide.

11. (Amended) An expression cassette, comprising a nucleic acid fragment or a sequence according to ~~one of claimsclaim~~ 1-~~to 9~~, together with at least one control or regulatory sequence.

13. (Amended) An expression cassette according to ~~one of claims~~claim 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. (Amended) Use of nucleic acid sequences according to ~~claims~~claim 1 to 10 for producing full-length genes.

16. (Amended) Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to ~~one of claims~~claim 1 to 10.

18. (Amended) Host cell according to ~~one of claims~~claim 16 or 17, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. (Amended) A process for producing a polypeptide or a fragment, wherein the host cells according to claim 16 to 18 are cultivated.

27. (Amended) Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as tools for finding active ingredients against the bladder tumor.

28. (Amended) Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. (Amended) Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of claim 2 in sense or antisense form.

30. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. (Amended) Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 of claim 23 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. (Amended) Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431 of claim 23.

33. (Amended) A nucleic acid sequence according to ~~claims~~claim 1-~~to 10~~, wherein it is a genomic sequence.

34. (Amended) A nucleic acid sequence according to ~~claims~~claim 1-~~to 10~~, wherein it is an mRNA sequence.

35. (Amended) Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403 of claim 2.

38. (Amended) A nucleic acid sequence according to ~~claims~~claim 1-~~to 7~~, wherein the size of the fragment has a length of at least 300 to 3500 bp.

Human Nucleic Acid Sequences from Normal Bladder Tissue

The invention relates to human nucleic acid sequences from normal bladder tissue, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer is the bladder tumor, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer (> 2000 nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, which play a role as candidate genes in the bladder tumor, have now been found.

Nucleic acid sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, and 391-403 or a complementary or

allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, which are expressed elevated in the normal bladder tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-127 and 391-403.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-127 and 391-403 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia),
2. eukaryotic,



such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as *E. coli* or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols Seq. ID Nos. 128-390 and 404-431.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq ID Nos. 128-390 and 404-431 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-127 and 391-403 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 128-390 and 404-431 according to the invention can also be used as tools for finding active ingredients against the bladder tumor, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 for expression of polypeptides, which can be used as tools for finding active ingredients against the bladder tumor.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 as pharmaceutical agents in the gene therapy for treatment of bladder tumors or for the production of a pharmaceutical agent for treatment of bladder tumors.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained

from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-127 and 391-403, genomic BAC-, PAC- and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 for use as vehicles for gene transfer.

## Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

## Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

## Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

#### **Example 1**

##### **Search for Tumor-related Candidate Genes**

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the bladder tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.



**Example 2****Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

**2.1 Electronic Northern Blot**

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

**2.1.1**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 1 was found, which occurs 12.2 x more strongly in the normal bladder tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 1

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0312                | 0.0026               | 12.203        | 0.0819 |
| Breast               | 0.0064                | 0.0056               | 1.1342        | 0.8817 |
| Small intestine      | 0.0092                | 0.0000               | undef         | 0.0000 |
| Ovary                | 0.0060                | 0.0156               | 0.3838        | 2.6058 |
| Endocrine tissue     | 0.0068                | 0.0201               | 0.3396        | 2.9444 |
| Gastrointestinal     | 0.0096                | 0.0000               | undef         | 0.0000 |
| Brain                | 0.0111                | 0.0226               | 0.4909        | 2.0372 |
| Hematopoietic        | 0.0107                | 0.0379               | 0.2823        | 3.5422 |
| Skin                 | 0.0147                | 0.0000               | undef         | 0.0000 |
| Hepatic              | 0.0095                | 0.0000               | undef         | 0.0000 |
| Heart                | 0.0053                | 0.0000               | undef         | 0.0000 |
| Testicles            | 0.0173                | 0.0234               | 0.7380        | 1.3551 |
| Lung                 | 0.0083                | 0.0184               | 0.4516        | 2.2144 |
| Stomach-esophagus    | 0.0000                | 0.0230               | 0.0000        | undef  |
| Muscle-skeleton      | 0.0120                | 0.0120               | 0.9994        | 1.0006 |
| Kidney               | 0.0081                | 0.0274               | 0.2974        | 3.3626 |
| Pancreas             | 0.0083                | 0.0110               | 0.7479        | 1.3371 |
| Penis                | 0.0120                | 0.0000               | undef         | 0.0000 |
| Prostate             | 0.0044                | 0.0106               | 0.4095        | 2.4423 |
| Uterus-endometrium   | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-myometrium    | 0.0152                | 0.0204               | 0.7482        | 1.3366 |
| Uterus-general       | 0.0051                | 0.0000               | undef         | 0.0000 |
| Breast hyperplasia   | 0.0096                |                      |               |        |
| Prostate hyperplasia | 0.0000                |                      |               |        |
| Seminal vesicle      | 0.0000                |                      |               |        |
| Sensory organs       | 0.0139                |                      |               |        |
| White blood cells    | 0.0000                |                      |               |        |
| Cervix               |                       |                      |               |        |

|                     | FETUS<br>% frequency | STANDARDIZED/SUBTRACTED<br>LIBRARIES<br>% frequency |        |
|---------------------|----------------------|---|--------|
| Development         | 0.0000               | Breast  | 0.0000 |
| Gastrointestinal    | 0.0083               | Ovary_n   | 0.0000 |
| Brain               | 0.0063               | Ovary_t   | 0.0051 |
| Hematopoietic       | 0.0157               | Endocrine tissue                                    | 0.0000 |
| Skin                | 0.0000               | Fetal   | 0.0035 |
| Hepatic             | 0.0000               | Gastrointestinal                                    | 0.0122 |
| Heart-blood vessels | 0.0107               | Hematopoietic                                       | 0.0171 |
| Lung                | 0.0253               | Skin-muscle   | 0.0065 |
| Suprarenal gland    | 0.0507               | Testicles   | 0.0077 |
| Kidney              | 0.0000               | Lung  | 0.0082 |
| Placenta            | 0.0182               | Nerves  | 0.0090 |
| Prostate            | 0.0000               | Prostate  | 0.0068 |
| Sensory organs      | 0.0377               | Sensory Organs                                      | 0.0000 |
|                     |                      | Uterus_n  | 0.0042 |

In an analogous procedure, the following Northernblots were also found:

| Electronic Northern for SEQ. ID NO.: 2 |             |             |        |        |
|--|-------------|-------------|--------|--------|
|  | NORMAL      | TUMOR       | Ratios |        |
|  | % frequency | % frequency | N/T    | T/N    |
| Bladder                                | 0.0741      | 0.0102      | 7.2459 | 0.1380 |
| Breast                                 | 0.0102      | 0.0038      | 2.7221 | 0.3674 |
| Small intestine                        | 0.0061      | 0.0000      | undef  | 0.0000 |
| Ovary                                  | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue                       | 0.0017      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal                       | 0.0038      | 0.0046      | 0.8283 | 1.2072 |
| Brain                                  | 0.0007      | 0.0021      | 0.3600 | 2.7779 |
| Hematopoietic                          | 0.0000      | 0.0000      | undef  | undef  |
| Skin                                   | 0.0184      | 0.0000      | undef  | 0.0000 |
| Hepatic                                | 0.0000      | 0.0000      | undef  | undef  |
| Heart                                  | 0.0032      | 0.0000      | undef  | 0.0000 |
| Testicles                              | 0.0058      | 0.0000      | undef  | 0.0000 |
| Lung                                   | 0.0052      | 0.0061      | 0.8467 | 1.1810 |
| Stomach-esophagus                      | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton                        | 0.0034      | 0.0060      | 0.5711 | 1.7510 |
| Kidney                                 | 0.0027      | 0.0068      | 0.3965 | 2.5219 |
| Pancreas                               | 0.0017      | 0.0055      | 0.2991 | 3.3428 |
| Penis                                  | 0.0170      | 0.0267      | 0.4493 | 2.2259 |
| Prostate                               | 0.0109      | 0.0064      | 1.7060 | 0.5862 |
| Uterus-endometrium                     | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium                      | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general                         | 0.0051      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia                     | 0.0064      |             |        |        |
| Prostate hyperplasia                   | 0.0030      |             |        |        |
| Seminal vesicle                        | 0.0000      |             |        |        |
| Sensory organs                         | 0.0052      |             |        |        |
| White blood cells                      | 0.0000      |             |        |        |
| Cervix                                 |             |             |        |        |

| FETUS               |             | STANDARDIZED/SUBTRACTED |             |
|---------------------|-------------|-------------------------|-------------|
|                     | % frequency | LIBRARIES               | % frequency |
| Development         | 0.0278      | Breast                  | 0.0068      |
| Gastrointestinal    | 0.0028      | Ovary_n                 | 0.0000      |
| Brain               | 0.0000      | Ovary_t                 | 0.0000      |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000      |
| Skin                | 0.0000      | Fetal                   | 0.0012      |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000      |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000      |
| Lung                | 0.0036      | Skin-muscle             | 0.0032      |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000      |
| Kidney              | 0.0000      | Lung                    | 0.0000      |
| Placenta            | 0.0061      | Nerves                  | 0.0010      |
| Prostate            | 0.0000      | Prostate                | 0.0068      |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000      |
|                     |             | Uterus_n                | 0.0042      |

## Electronic Northern for SEQ. ID NO.: 3

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0585      | 0.0153      | 3.8136 | 0.2622 |
| Breast               | 0.0064      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0184      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0000      | 0.0026      | 0.0000 | undef  |
| Endocrine tissue     | 0.0204      | 0.0100      | 2.0377 | 0.4907 |
| Gastrointestinal     | 0.0077      | 0.0046      | 1.6567 | 0.6036 |
| Brain                | 0.0059      | 0.0092      | 0.6400 | 1.5626 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0065      | 0.0000 | undef  |
| Heart                | 0.0085      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0173      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0104      | 0.0020      | 5.0803 | 0.1968 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0017      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0217      | 0.0068      | 3.1722 | 0.3152 |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0060      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0654      | 0.0362      | 1.8064 | 0.5536 |
| Uterus-endometrium   | 0.0135      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0076      | 0.0204      | 0.3741 | 2.6732 |
| Uterus-general       | 0.0000      | 0.1908      | 0.0000 | undef  |
| Breast hyperplasia   | 0.0032      |             |        |        |
| Prostate hyperplasia | 0.0803      |             |        |        |
| Seminal vesicle      | 0.0178      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               | 0.0106      |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0139 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0083 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0128 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0162 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0124 | Lung             | 0.0164 |
| Placenta            | 0.0000 | Nerves           | 0.0050 |
| Prostate            | 0.0000 | Prostate         | 0.0205 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0333 |

## Electronic Northern for SEQ. ID NO.: 4

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0351      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.3000      | 0.0010      | 0.0000 | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 6

|                      | NORMAL      | TUMOR       | Ratios  |        |
|----------------------|-------------|-------------|---------|--------|
|                      | % frequency | % frequency | N/T     | T/N    |
| Bladder              | 0.0390      | 0.0026      | 15.2544 | 0.0656 |
| Breast               | 0.0460      | 0.0056      | 8.1663  | 0.1225 |
| Small intestine      | 0.0123      | 0.0331      | 0.3707  | 2.6973 |
| Ovary                | 0.0000      | 0.0052      | 0.0000  | undef  |
| Endocrine tissue     | 0.0119      | 0.0050      | 2.3774  | 0.4206 |
| Gastrointestinal     | 0.0038      | 0.0000      | undef   | 0.0000 |
| Brain                | 0.0052      | 0.0072      | 0.7200  | 1.3890 |
| Hematopoietic        | 0.0013      | 0.0000      | undef   | 0.0000 |
| Skin                 | 0.0294      | 0.0000      | undef   | 0.0000 |
| Hepatic              | 0.0143      | 0.0065      | 2.2059  | 0.4533 |
| Heart                | 0.0074      | 0.0000      | undef   | 0.0000 |
| Testicles            | 0.0058      | 0.0117      | 0.4920  | 2.0326 |
| Lung                 | 0.0021      | 0.0000      | undef   | 0.0000 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef   | undef  |
| Muscle-skeleton      | 0.0103      | 0.0240      | 0.4283  | 2.3347 |
| Kidney               | 0.0516      | 0.0000      | undef   | 0.0000 |
| Pancreas             | 0.0000      | 0.0000      | undef   | undef  |
| Penis                | 0.0090      | 0.0000      | undef   | 0.0000 |
| Prostate             | 0.0044      | 0.0064      | 0.6824  | 1.4654 |
| Uterus-endometrium   | 0.0270      | 0.0000      | undef   | 0.0000 |
| Uterus-myometrium    | 0.0381      | 0.0000      | undef   | 0.0000 |
| Uterus-general       | 0.0000      | 0.0000      | undef   | undef  |
| Breast hyperplasia   | 0.1087      |             |         |        |
| Prostate hyperplasia | 0.0059      |             |         |        |
| Seminal vesicle      | 0.0089      |             |         |        |
| Sensory organs       | 0.0000      |             |         |        |
| White blood cells    | 0.0000      |             |         |        |
| Cervix               | 0.0319      |             |         |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         |             | Breast                  | 0.0272 |
| Gastrointestinal    | 0.0557      | Ovary_n                 | 0.0000 |
| Brain               | 0.0028      | Ovary_t                 | 0.0101 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0116 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000 |
| Lung                | 0.0498      | Skin-muscle             | 0.0194 |
| Suprarenal gland    | 0.0036      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0000 |
| Placenta            | 0.0000      | Nerves                  | 0.0151 |
| Prostate            | 0.0000      | Prostate                | 0.0000 |
| Sensory organs      | 0.0251      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0208 |

## Electronic Northern for SEQ. ID NO.: 7

|                      | NORMAL      | TUMOR       | Ratios  |        |
|----------------------|-------------|-------------|---------|--------|
|                      | % frequency | % frequency | N/T     | T/N    |
| Bladder              | 0.0351      | 0.0025      | 13.7290 | 0.0729 |
| Breast               | 0.0051      | 0.0038      | 1.3611  | 0.7347 |
| Small intestine      | 0.0000      | 0.0000      | undef   | undef  |
| Ovary                | 0.0060      | 0.0000      | undef   | 0.0000 |
| Endocrine tissue     | 0.0034      | 0.0000      | undef   | 0.0000 |
| Gastrointestinal     | 0.0057      | 0.0046      | 1.2425  | 0.8049 |
| Brain                | 0.0044      | 0.0000      | undef   | 0.0000 |
| Hematopoietic        | 0.0053      | 0.0000      | undef   | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef   | undef  |
| Hepatic              | 0.0048      | 0.0000      | undef   | 0.0000 |
| Heart                | 0.0021      | 0.0137      | 0.1542  | 6.4853 |
| Testicles            | 0.0000      | 0.0117      | 0.0000  | undef  |
| Lung                 | 0.0021      | 0.0020      | 1.0161  | 0.9842 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef   | undef  |
| Muscle-skeleton      | 0.0017      | 0.0000      | undef   | 0.0000 |
| Kidney               | 0.0000      | 0.0000      | undef   | undef  |
| Pancreas             | 0.0000      | 0.0055      | 0.0000  | undef  |
| Penis                | 0.0030      | 0.0000      | undef   | 0.0000 |
| Prostate             | 0.0044      | 0.0021      | 2.0473  | 0.4885 |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef   | 0.0000 |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef   | undef  |
| Uterus-general       | 0.0051      | 0.0000      | undef   | 0.0000 |
| Breast hyperplasia   | 0.0032      |             |         |        |
| Prostate hyperplasia | 0.0000      |             |         |        |
| Seminal vesicle      | 0.0000      |             |         |        |
| Sensory organs       | 0.0035      |             |         |        |
| White blood cells    | 0.0000      |             |         |        |
| Cervix               |             |             |         |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0063 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0047 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0063 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0062 | Lung             | 0.0040 |
| Placenta            | 0.0061 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0042 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 8

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0234      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0013      | 0.0019      | 0.6805 | 1.4694 |
| Small intestine      | 0.0061      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0000      | 0.0026      | 0.0000 | undef  |
| Endocrine tissue     | 0.0034      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0022      | 0.0051      | 0.4320 | 2.3149 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0048      | 0.0000      | undef  | 0.0000 |
| Heart                | 0.0042      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0041      | 0.0000 | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0051      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0017      | 0.0055      | 0.2991 | 3.3428 |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0065      | 0.0043      | 1.5354 | 0.6513 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0032      |             |        |        |
| Prostate hyperplasia | 0.0059      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0026      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0139 | Breast           | 0.0068 |
| Gastrointestinal    | 0.0028 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0039 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0012 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0032 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0082 |
| Placenta            | 0.0000 | Nerves           | 0.0040 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0083 |



## Electronic Northern for SEQ. ID NO.: 9

|                      | NORMAL      | TUMOR       | Ratios  |        |
|----------------------|-------------|-------------|---------|--------|
|                      | % frequency | % frequency | N/T     | T/N    |
| Bladder              | 0.0273      | 0.0026      | 10.6781 | 0.0936 |
| Breast               | 0.0026      | 0.0019      | 1.3611  | 0.7347 |
| Small intestine      | 0.0061      | 0.0000      | undef   | 0.0000 |
| Ovary                | 0.0060      | 0.0052      | 1.1513  | 0.8686 |
| Endocrine tissue     | 0.0051      | 0.0000      | undef   | 0.0000 |
| Gastrointestinal     | 0.0038      | 0.0046      | 0.8283  | 1.2072 |
| Brain                | 0.0037      | 0.0051      | 0.7200  | 1.3890 |
| Hematopoietic        | 0.0000      | 0.0379      | 0.0000  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef   | undef  |
| Hepatic              | 0.0000      | 0.0065      | 0.0000  | undef  |
| Heart                | 0.0000      | 0.0000      | undef   | undef  |
| Testicles            | 0.0000      | 0.0117      | 0.0000  | undef  |
| Lung                 | 0.0042      | 0.0020      | 2.0321  | 0.4921 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef   | undef  |
| Muscle-skeleton      | 0.0051      | 0.0060      | 0.8567  | 1.1673 |
| Kidney               | 0.0027      | 0.0000      | undef   | 0.0000 |
| Pancreas             | 0.0017      | 0.0000      | undef   | 0.0000 |
| Penis                | 0.0000      | 0.0267      | 0.0000  | undef  |
| Prostate             | 0.0000      | 0.0085      | 0.0000  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef   | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef   | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef   | undef  |
| Breast hyperplasia   | 0.0030      |             |         |        |
| Prostate hyperplasia | 0.0000      |             |         |        |
| Seminal vesicle      | 0.0000      |             |         |        |
| Sensory organs       | 0.0052      |             |         |        |
| White blood cells    | 0.0000      |             |         |        |
| Cervix               |             |             |         |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0101 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0490 |
| Skin                | 0.0000 | Fetal            | 0.0017 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0114 |
| Lung                | 0.0036 | Skin-muscle      | 0.0194 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0061 | Nerves           | 0.0040 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 12

|                      | NORMAL      | TUMOR       | Ratios | T/N    |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    |        |
| Bladder              | 0.0858      | 0.0358      | 2.3971 | 0.4172 |
| Breast               | 0.0435      | 0.0338      | 1.2854 | 0.7779 |
| Small intestine      | 0.0276      | 0.0165      | 1.6683 | 0.5994 |
| Ovary                | 0.0120      | 0.0182      | 0.6579 | 1.5201 |
| Endocrine tissue     | 0.0290      | 0.0176      | 1.6496 | 0.6062 |
| Gastrointestinal     | 0.0594      | 0.0231      | 2.5679 | 0.3894 |
| Brain                | 0.0333      | 0.0657      | 0.5062 | 1.9754 |
| Hematopoietic        | 0.0134      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0514      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0381      | 0.0123      | 2.9412 | 0.3400 |
| Heart                | 0.0413      | 0.0275      | 1.5034 | 0.6652 |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0384      | 0.0164      | 2.3497 | 0.4256 |
| Stomach-esophagus    | 0.0290      | 0.0307      | 0.9454 | 1.0578 |
| Muscle-skeleton      | 0.0188      | 0.0360      | 0.5235 | 1.9102 |
| Kidney               | 0.0217      | 0.0548      | 0.3965 | 2.5219 |
| Pancreas             | 0.0132      | 0.0166      | 0.7977 | 1.2536 |
| Penis                | 0.0779      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0632      | 0.0447      | 1.4136 | 0.7074 |
| Uterus-endometrium   | 0.0135      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0229      | 0.0068      | 3.3669 | 0.2970 |
| Uterus-general       | 0.0306      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0416      |             |        |        |
| Prostate hyperplasia | 0.0595      |             |        |        |
| Seminal vesicle      | 0.0712      |             |        |        |
| Sensory organs       | 0.0118      |             |        |        |
| White blood cells    | 0.0087      |             |        |        |
| Cervix               | 0.0426      |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.1293 |
| Gastrointestinal    | 0.0250 | Ovary_n          | 0.1595 |
| Brain               | 0.0063 | Ovary_t          | 0.0101 |
| Hematopoietic       | 0.0118 | Endocrine tissue | 0.0490 |
| Skin                | 0.0000 | Fetal            | 0.0338 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0036 | Hematopoietic    | 0.0000 |
| Lung                | 0.0108 | Skin-muscle      | 0.0162 |
| Suprarenal gland    | 0.1014 | Testicles        | 0.0000 |
| Kidney              | 0.0185 | Lung             | 0.0301 |
| Placenta            | 0.0242 | Nerves           | 0.0410 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0628 | Sensory Organs   | 0.0624 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 13

|                      | NORMAL      | TUMOR       | Ratios | T/N    |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    |        |
| Bladder              | 0.0468      | 0.0077      | 6.1018 | 0.1639 |
| Breast               | 0.0294      | 0.0075      | 3.9130 | 0.2556 |
| Small intestine      | 0.0184      | 0.0165      | 1.1122 | 0.8991 |
| Ovary                | 0.0090      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0085      | 0.0050      | 1.6981 | 0.5889 |
| Gastrointestinal     | 0.0192      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0059      | 0.0062      | 0.9599 | 1.0417 |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0808      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0065      | 0.0000 | undef  |
| Heart                | 0.0540      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0156      | 0.0082      | 1.9051 | 0.5249 |
| Stomach-esophagus    | 0.0193      | 0.0077      | 2.5211 | 0.3967 |
| Muscle-skeleton      | 0.1216      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0000      | 0.0274      | 0.0000 | undef  |
| Pancreas             | 0.0000      | 0.0055      | 0.0000 | undef  |
| Penis                | 0.1587      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0087      | 0.0106      | 0.8189 | 1.2211 |
| Uterus-endometrium   | 0.0338      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0457      | 0.0272      | 1.6834 | 0.5940 |
| Uterus-general       | 0.0357      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0160      |             |        |        |
| Prostate hyperplasia | 0.0208      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0009      |             |        |        |
| White blood cells    | 0.0426      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0167 |
| Brain               | 0.0063 |
| Hematopoietic       | 0.0039 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0249 |
| Lung                | 0.0108 |
| Suprarenal gland    | 0.0254 |
| Kidney              | 0.0062 |
| Placenta            | 0.0000 |
| Prostate            | 0.0249 |
| Sensory organs      | 0.0000 |

|                  |        |
|------------------|--------|
| Breast           | 0.0000 |
| Ovary_n          | 0.0000 |
| Ovary_t          | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal            | 0.0029 |
| Gastrointestinal | 0.0244 |
| Hematopoietic    | 0.0000 |
| Skin-muscle      | 0.0032 |
| Testicles        | 0.0309 |
| Lung             | 0.0082 |
| Nerves           | 0.0090 |
| Prostate         | 0.0000 |
| Sensory Organs   | 0.0077 |
| Uterus_n         | 0.0208 |

## Electronic Northern for SEQ. ID NO.: 14

|                      | NORMAL      | TUMOR       | Ratios  |        |
|----------------------|-------------|-------------|---------|--------|
|                      | % frequency | % frequency | N/T     | T/N    |
| Bladder              | 0.0351      | 0.0026      | 13.7290 | 0.0728 |
| Breast               | 0.0102      | 0.0075      | 1.3611  | 0.7347 |
| Small intestine      | 0.0092      | 0.0000      | undef   | 0.0000 |
| Ovary                | 0.0090      | 0.0026      | 3.4538  | 0.2895 |
| Endocrine tissue     | 0.0051      | 0.0025      | 2.0377  | 0.4907 |
| Gastrointestinal     | 0.0115      | 0.0000      | undef   | 0.0000 |
| Brain                | 0.0000      | 0.0000      | undef   | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef   | undef  |
| Skin                 | 0.0073      | 0.0000      | undef   | 0.0000 |
| Hepatic              | 0.0048      | 0.0065      | 0.7353  | 1.3600 |
| Heart                | 0.0233      | 0.0137      | 1.6961  | 0.5896 |
| Testicles            | 0.0000      | 0.0000      | undef   | undef  |
| Lung                 | 0.0135      | 0.0041      | 3.3022  | 0.3028 |
| Stomach-esophagus    | 0.0193      | 0.0000      | undef   | 0.0000 |
| Muscle-skeleton      | 0.0634      | 0.0000      | undef   | 0.0000 |
| Kidney               | 0.0027      | 0.0068      | 0.3965  | 2.5219 |
| Pancreas             | 0.0017      | 0.0000      | undef   | 0.0000 |
| Penis                | 0.0359      | 0.0000      | undef   | 0.0000 |
| Prostate             | 0.0218      | 0.0043      | 5.1181  | 0.1954 |
| Uterus-endometrium   | 0.0203      | 0.0000      | undef   | 0.0000 |
| Uterus-myometrium    | 0.0229      | 0.0000      | undef   | 0.0000 |
| Uterus-general       | 0.0255      | 0.0000      | undef   | 0.0000 |
| Breast hyperplasia   | 0.0000      |             |         |        |
| Prostate hyperplasia | 0.0089      |             |         |        |
| Seminal vesicle      | 0.0089      |             |         |        |
| Sensory organs       | 0.0000      |             |         |        |
| White blood cells    | 0.0000      |             |         |        |
| Cervix               |             |             |         |        |

| FETUS               |        | STANDARDIZED/SUBTRACTED |        |
|---------------------|--------|-------------------------|--------|
| % frequency         |        | LIBRARIES               |        |
|                     |        | % frequency             |        |
| Development         | 0.0000 | Breast                  | 0.0136 |
| Gastrointestinal    | 0.0139 | Ovary_n                 | 0.0000 |
| Brain               | 0.0000 | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0039 | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000 | Fetal                   | 0.0029 |
| Hepatic             | 0.0000 | Gastrointestinal        | 0.0244 |
| Heart-blood vessels | 0.0071 | Hematopoietic           | 0.0000 |
| Lung                | 0.0000 | Skin-muscle             | 0.0000 |
| Suprarenal gland    | 0.0507 | Testicles               | 0.0000 |
| Kidney              | 0.0062 | Lung                    | 0.0000 |
| Placenta            | 0.0000 | Nerves                  | 0.0181 |
| Prostate            | 0.0000 | Prostate                | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs          | 0.0000 |
|                     |        | Uterus_n                | 0.0583 |

## Electronic Northern for SEQ. ID NO.: 17

|                      | NORMAL      | TUMOR       | Ratios  | T/N    |
|----------------------|-------------|-------------|---------|--------|
|                      | % frequency | % frequency | N/T     |        |
| Bladder              | 0.0273      | 0.0026      | 10.6781 | 0.0936 |
| Breast               | 0.0307      | 0.0038      | 8.1663  | 0.1225 |
| Small intestine      | 0.0061      | 0.0165      | 0.3707  | 2.6973 |
| Ovary                | 0.0030      | 0.0000      | undef   | 0.0000 |
| Endocrine tissue     | 0.0000      | 0.0025      | 0.0000  | undef  |
| Gastrointestinal     | 0.0249      | 0.0000      | undef   | 0.0000 |
| Brain                | 0.0015      | 0.0010      | 1.4399  | 0.6945 |
| Hematopoietic        | 0.0040      | 0.0000      | undef   | 0.0000 |
| Skin                 | 0.0367      | 0.0000      | undef   | 0.0000 |
| Hepatic              | 0.0000      | 0.0065      | 0.0000  | undef  |
| Heart                | 0.0148      | 0.0000      | undef   | 0.0000 |
| Testicles            | 0.0058      | 0.0000      | undef   | 0.0000 |
| Lung                 | 0.0062      | 0.0020      | 3.0482  | 0.3281 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef   | undef  |
| Muscle-skeleton      | 0.0274      | 0.0000      | undef   | 0.0000 |
| Kidney               | 0.0000      | 0.0000      | undef   | undef  |
| Pancreas             | 0.0050      | 0.0000      | undef   | 0.0000 |
| Penis                | 0.0120      | 0.0267      | 0.4493  | 2.2259 |
| Prostate             | 0.0087      | 0.0000      | undef   | 0.0000 |
| Uterus-endometrium   | 0.0135      | 0.0000      | undef   | 0.0000 |
| Uterus-myometrium    | 0.0229      | 0.0000      | undef   | 0.0000 |
| Uterus-general       | 0.0000      | 0.0000      | undef   | undef  |
| Breast hyperplasia   | 0.0288      |             |         |        |
| Prostate hyperplasia | 0.0030      |             |         |        |
| Seminal vesicle      | 0.0000      |             |         |        |
| Sensory organs       | 0.0118      |             |         |        |
| White blood cells    | 0.0000      |             |         |        |
| Cervix               | 0.0106      |             |         |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development 0.0000  
Gastrointestinal 0.0111  
Brain 0.0000  
Hematopoietic 0.0039  
Skin 0.0000  
Hepatic 0.0000  
Heart-blood vessels 0.0036  
Lung 0.0000  
Suprarenal gland 0.0000  
Kidney 0.0062  
Placenta 0.0000  
Prostate 0.0000  
Sensory organs 0.0000

Breast 0.0204  
Ovary\_n 0.0000  
Ovary\_t 0.0051  
Endocrine tissue 0.0000  
Fetal 0.0047  
Gastrointestinal 0.0000  
Hematopoietic 0.0000  
Skin-muscle 0.0000  
Testicles 0.0000  
Lung 0.0000  
Nerves 0.0000  
Prostate 0.0000  
Sensory Organs 0.0083  
Uterus\_n

## Electronic Northern for SEQ. ID NO.: 18

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0585      | 0.0230      | 2.5424 | 0.3933 |
| Breast               | 0.0013      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0368      | 0.0165      | 2.2244 | 0.4496 |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0051      | 0.0025      | 2.0377 | 0.4907 |
| Gastrointestinal     | 0.0115      | 0.0046      | 2.4850 | 0.4024 |
| Brain                | 0.0022      | 0.0031      | 0.7200 | 1.3890 |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0110      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0095      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0020      | 0.0000 | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0051      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0017      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0509      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0218      | 0.0149      | 1.4623 | 0.6838 |
| Prostate             | 0.0058      | 0.0000      | undef  | 0.0000 |
| Uterus-endometrium   | 0.0229      | 0.0543      | 0.4208 | 2.3761 |
| Uterus-myometrium    | 0.0407      | 0.0000      | undef  | 0.0000 |
| Uterus-general       | 0.0012      |             |        |        |
| Breast hyperplasia   | 0.0059      |             |        |        |
| Prostate hyperplasia | 0.0356      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0106      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0068 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0052 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic    | 0.0000 |
| Lung                | 0.0108 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0030 |
| Placenta            | 0.0000 | Nerves           | 0.0137 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0083 |
|                     |        | Uterus_n         |        |

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## Electronic Northern for SEQ. ID NO.: 20

|                      | NORMAL      | TUMOR       | Ratios | T/N     |
|----------------------|-------------|-------------|--------|---------|
|                      | % frequency | % frequency | N/T    |         |
| Bladder              | 0.0429      | 0.0153      | 2.7965 | 0.3576  |
| Breast               | 0.0141      | 0.0282      | 0.4991 | 2.0038  |
| Small intestine      | 0.0307      | 0.0165      | 1.8537 | 0.5395  |
| Ovary                | 0.0300      | 0.0390      | 0.7675 | 1.3029  |
| Endocrine tissue     | 0.0409      | 0.0176      | 2.3288 | 0.4294  |
| Gastrointestinal     | 0.0230      | 0.0139      | 1.6567 | 0.6036  |
| Brain                | 0.0200      | 0.0298      | 0.6703 | 1.4919  |
| Hematopoietic        | 0.0160      | 0.0000      | undef  | 0.0000  |
| Skin                 | 0.0257      | 0.0000      | undef  | 0.0000  |
| Hepatic              | 0.0143      | 0.0259      | 0.5515 | 1.8133  |
| Heart                | 0.0339      | 0.0000      | undef  | 0.0000  |
| Testicles            | 0.0288      | 0.0234      | 1.2299 | 0.8130  |
| Lung                 | 0.0270      | 0.0409      | 0.6604 | 1.5141  |
| Stomach-esophagus    | 0.0483      | 0.0230      | 2.1009 | 0.4740  |
| Muscle-skeleton      | 0.0394      | 0.0240      | 1.6419 | 0.6090  |
| Kidney               | 0.0244      | 0.0205      | 1.1896 | 0.8406  |
| Pancreas             | 0.0198      | 0.0276      | 0.7180 | 1.3928  |
| Penis                | 0.0359      | 0.0533      | 0.6739 | 1.4839  |
| Prostate             | 0.0305      | 0.0255      | 1.1942 | 0.8374  |
| Uterus-endometrium   | 0.0270      | 0.0000      | undef  | 0.0000  |
| Uterus-myometrium    | 0.0534      | 0.0272      | 1.9640 | 0.5092  |
| Uterus-general       | 0.0051      | 0.0954      | 0.0534 | 18.7357 |
| Breast hyperplasia   | 0.0384      |             |        |         |
| Prostate hyperplasia | 0.0595      |             |        |         |
| Seminal vesicle      | 0.0267      |             |        |         |
| Sensory organs       | 0.0118      |             |        |         |
| White blood cells    | 0.0286      |             |        |         |
| Cervix               | 0.0426      |             |        |         |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0222 | Ovary_n          | 0.0000 |
| Brain               | 0.0063 | Ovary_t          | 0.0051 |
| Hematopoietic       | 0.0079 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0006 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0285 | Skin-muscle      | 0.0065 |
| Suprarenal gland    | 0.0470 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0082 |
| Placenta            | 0.0247 | Nerves           | 0.0080 |
| Prostate            | 0.0121 | Prostate         | 0.0205 |
| Sensory organs      | 0.0249 | Sensory Organs   | 0.0000 |
|                     | 0.0377 | Uterus_n         | 0.0250 |

## Electronic Northern for SEQ. ID NO.: 21

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0195      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0026      | 0.0019      | 1.3611 | 0.7347 |
| Small intestine      | 0.0061      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0000      | 0.0052      | 0.0000 | undef  |
| Endocrine tissue     | 0.0034      | 0.0150      | 0.2264 | 4.4166 |
| Gastrointestinal     | 0.0000      | 0.0139      | 0.0000 | undef  |
| Brain                | 0.0177      | 0.0031      | 5.7597 | 0.1736 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0048      | 0.0000      | undef  | 0.0000 |
| Heart                | 0.0064      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0117      | 0.0000 | undef  |
| Lung                 | 0.0031      | 0.0123      | 0.2540 | 3.9367 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0017      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0027      | 0.0068      | 0.3965 | 2.5219 |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0120      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0000      | 0.0021      | 0.0000 | undef  |
| Uterus-endometrium   | 0.0135      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0076      | 0.0068      | 1.1223 | 0.8911 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0032      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0009      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0012 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0142 | Hematopoietic    | 0.0000 |
| Lung                | 0.0036 | Skin-muscle      | 0.0065 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0070 |
| Placenta            | 0.0061 | Nerves           | 0.0068 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0125 |
|                     |        | Uterus_n         |        |



## Electronic Northern for SEQ. ID NO.: 22

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0156                | 0.0000               | undef         | 0.0000 |
| Breast               | 0.0013                | 0.0019               | 0.6805        | 1.4694 |
| Small intestine      | 0.0031                | 0.0000               | undef         | 0.0000 |
| Ovary                | 0.0000                | 0.0026               | 0.0000        | undef  |
| Endocrine tissue     | 0.0017                | 0.0000               | undef         | 0.0000 |
| Gastrointestinal     | 0.0019                | 0.0000               | undef         | 0.0000 |
| Brain                | 0.0007                | 0.0021               | 0.3600        | 2.7779 |
| Hematopoietic        | 0.0000                | 0.0000               | undef         | undef  |
| Skin                 | 0.0000                | 0.0000               | undef         | undef  |
| Hepatic              | 0.0000                | 0.0065               | 0.0000        | undef  |
| Heart                | 0.0011                | 0.0000               | undef         | 0.0000 |
| Testicles            | 0.0000                | 0.0000               | undef         | undef  |
| Lung                 | 0.0000                | 0.0020               | 0.0000        | undef  |
| Stomach-esophagus    | 0.0000                | 0.0000               | undef         | undef  |
| Muscle-skeleton      | 0.0017                | 0.0000               | undef         | 0.0000 |
| Kidney               | 0.0027                | 0.0000               | undef         | 0.0000 |
| Pancreas             | 0.0000                | 0.0000               | undef         | undef  |
| Penis                | 0.0000                | 0.0000               | undef         | undef  |
| Prostate             | 0.0022                | 0.0000               | undef         | 0.0000 |
| Uterus-endometrium   | 0.0068                | 0.0000               | undef         | 0.0000 |
| Uterus-myometrium    | 0.0132                | 0.0068               | 2.2445        | 0.4453 |
| Uterus-general       | 0.0000                | 0.0000               | undef         | undef  |
| Breast hyperplasia   | 0.0032                |                      |               |        |
| Prostate hyperplasia | 0.0000                |                      |               |        |
| Seminal vesicle      | 0.0000                |                      |               |        |
| Sensory organs       | 0.0000                |                      |               |        |
| White blood cells    | 0.0009                |                      |               |        |
| Cervix               | 0.0000                |                      |               |        |

|                     | FETUS<br>% frequency | STANDARDIZED/SUBTRACTED<br>LIBRARIES<br>% frequency |        |
|---------------------|----------------------|---|--------|
| Development         | 0.0000               | Breast  | 0.0136 |
| Gastrointestinal    | 0.0028               | Ovary_n   | 0.0000 |
| Brain               | 0.0000               | Ovary_t   | 0.0000 |
| Hematopoietic       | 0.0000               | Endocrine tissue                                    | 0.0000 |
| Skin                | 0.0000               | Fetal   | 0.0023 |
| Hepatic             | 0.0000               | Gastrointestinal                                    | 0.0000 |
| Heart-blood vessels | 0.0000               | Hematopoietic                                       | 0.0000 |
| Lung                | 0.0000               | Skin-muscle   | 0.0000 |
| Suprarenal gland    | 0.0000               | Testicles   | 0.0000 |
| Kidney              | 0.0000               | Lung  | 0.0000 |
| Placenta            | 0.0000               | Nerves  | 0.0000 |
| Prostate            | 0.0000               | Prostate  | 0.0000 |
| Sensory organs      | 0.0000               | Sensory Organs                                      | 0.0000 |
|                     |                      | Uterus_n  |        |

## Electronic Northern for SEQ. ID NO.: 23

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0390      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0019      | 0.0000 | undef  |
| Small intestine      | 0.0153      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0017      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0115      | 0.0046      | 2.4950 | 0.4024 |
| Brain                | 0.0022      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0048      | 0.0000      | undef  | 0.0000 |
| Heart                | 0.0021      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0115      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0240      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0065      | 0.0064      | 1.0236 | 0.9769 |
| Uterus-endometrium   | 0.0338      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0229      | 0.0475      | 0.4910 | 2.0791 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0149      |             |        |        |
| Prostate hyperplasia | 0.0267      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0106      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0000      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0000 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000 |
| Lung                | 0.0000      | Skin-muscle             | 0.0000 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0000 |
| Placenta            | 0.0000      | Nerves                  | 0.0068 |
| Prostate            | 0.0249      | Prostate                | 0.0000 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                |        |

## Electronic Northern for SEQ. ID NO.: 24

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0351                | 0.0051               | 6.8645        | 0.1457 |
| Breast               | 0.0026                | 0.0056               | 0.4537        | 2.2042 |
| Small intestine      | 0.0092                | 0.0000               | undef         | 0.0000 |
| Ovary                | 0.0090                | 0.0130               | 0.6908        | 1.4477 |
| Endocrine tissue     | 0.0068                | 0.0075               | 0.9057        | 1.1042 |
| Gastrointestinal     | 0.0172                | 0.0139               | 1.2425        | 0.8048 |
| Brain                | 0.0044                | 0.0092               | 0.5400        | 1.8520 |
| Hematopoietic        | 0.0040                | 0.0000               | undef         | 0.0000 |
| Skin                 | 0.0037                | 0.0000               | undef         | 0.0000 |
| Hepatic              | 0.0000                | 0.0065               | 0.0000        | undef  |
| Heart                | 0.0074                | 0.0000               | undef         | 0.0000 |
| Testicles            | 0.0173                | 0.0117               | 1.4759        | 0.6775 |
| Lung                 | 0.0042                | 0.0143               | 0.2903        | 3.4446 |
| Stomach-esophagus    | 0.0000                | 0.0000               | undef         | undef  |
| Muscle-skeleton      | 0.0086                | 0.0060               | 1.4278        | 0.7004 |
| Kidney               | 0.0000                | 0.0205               | 0.0000        | undef  |
| Pancreas             | 0.0033                | 0.0110               | 0.2991        | 3.3428 |
| Penis                | 0.0180                | 0.0000               | undef         | 0.0000 |
| Prostate             | 0.0087                | 0.0128               | 0.6824        | 1.4654 |
| Uterus-endometrium   | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-myometrium    | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-general       | 0.0102                | 0.0000               | undef         | 0.0000 |
| Breast hyperplasia   | 0.0032                |                      |               |        |
| Prostate hyperplasia | 0.0119                |                      |               |        |
| Seminal vesicle      | 0.0000                |                      |               |        |
| Sensory organs       | 0.0118                |                      |               |        |
| White blood cells    | 0.0035                |                      |               |        |
| Cervix               | 0.0000                |                      |               |        |

FETUS  
% frequency

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0139 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0000 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0071 |
| Lung                | 0.0036 |
| Suprarenal gland    | 0.0254 |
| Kidney              | 0.0062 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                  |        |
|------------------|--------|
| Breast           | 0.0000 |
| Ovary_n          | 0.0000 |
| Ovary_t          | 0.0101 |
| Endocrine tissue | 0.0000 |
| Fetal            | 0.0181 |
| Gastrointestinal | 0.0000 |
| Hematopoietic    | 0.0114 |
| Skin-muscle      | 0.0130 |
| Testicles        | 0.0154 |
| Lung             | 0.0082 |
| Nerves           | 0.0060 |
| Prostate         | 0.0068 |
| Sensory Organs   | 0.0000 |
| Uterus_n         | 0.0416 |

## Electronic Northern for SEQ. ID NO.: 25

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0234      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      |             |        |        |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0028 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 26

|                      | NORMAL      | TUMOR       | Ratios | T/N    |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    |        |
| Bladder              | 0.0429      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0013      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0030      | 0.0026      | 1.1513 | 0.8686 |
| Endocrine tissue     | 0.0034      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0015      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0011      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0077      | 0.0000 | undef  |
| Muscle-skeleton      | 0.0017      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0054      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0090      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0000      | 0.0043      | 0.0000 | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0076      | 0.0000      | undef  | 0.0000 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0089      |             |        |        |
| Seminal vesicle      | 0.0235      |             |        |        |
| Sensory organs       | 0.0026      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0139 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0245 |
| Skin                | 0.0000 | Fetal            | 0.0012 |
| Hepatic             | 0.0260 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic    | 0.0171 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0042 |
|                     |        | Uterus_n         |        |

| Electronic Northern for SEQ. ID NO.: 27 |             |             |        |        |
|---|-------------|-------------|--------|--------|
|   | NORMAL      | TUMOR       | Ratios | T/N    |
|   | % frequency | % frequency | N/T    |        |
| Bladder                                 | 0.0312      | 0.0000      | undef  | 0.0000 |
| Breast                                  | 0.0090      | 0.0056      | 1.5879 | 0.6298 |
| Small intestine                         | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                                   | 0.0060      | 0.0052      | 1.1513 | 0.8686 |
| Endocrine tissue                        | 0.0034      | 0.0075      | 0.4528 | 2.2083 |
| Gastrointestinal                        | 0.0077      | 0.0000      | undef  | 0.0000 |
| Brain                                   | 0.0030      | 0.0051      | 0.5760 | 1.7362 |
| Hematopoietic                           | 0.0000      | 0.0000      | undef  | undef  |
| Skin                                    | 0.0048      | 0.0000      | undef  | 0.0000 |
| Hepatic                                 | 0.0021      | 0.0000      | undef  | 0.0000 |
| Heart                                   | 0.0000      | 0.0000      | undef  | undef  |
| Testicles                               | 0.0010      | 0.0020      | 0.5080 | 1.9684 |
| Lung                                    | 0.0290      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus                       | 0.0017      | 0.0000      | undef  | 0.0000 |
| Muscle-skeleton                         | 0.0054      | 0.0068      | 0.7930 | 1.2610 |
| Kidney                                  | 0.0017      | 0.0000      | undef  | 0.0000 |
| Pancreas                                | 0.0090      | 0.0000      | undef  | 0.0000 |
| Penis                                   | 0.0065      | 0.0043      | 1.5354 | 0.6513 |
| Prostate                                | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium                      | 0.0132      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium                       | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general                          | 0.0000      |             |        |        |
| Breast hyperplasia                      | 0.0059      |             |        |        |
| Prostate hyperplasia                    | 0.0000      |             |        |        |
| Seminal vesicle                         | 0.0000      |             |        |        |
| Sensory organs                          | 0.0009      |             |        |        |
| White blood cells                       | 0.0000      |             |        |        |
| Cervix                                  |             |             |        |        |

| FETUS               |        | STANDARDIZED/SUBTRACTED |        |
|---------------------|--------|-------------------------|--------|
| % frequency         |        | LIBRARIES               |        |
|                     |        | % frequency             |        |
| Development         | 0.0000 | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n                 | 0.0000 |
| Brain               | 0.0125 | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0039 | Endocrine tissue        | 0.0245 |
| Skin                | 0.0000 | Fetal                   | 0.0064 |
| Hepatic             | 0.0260 | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0071 | Hematopoietic           | 0.0114 |
| Lung                | 0.0000 | Skin-muscle             | 0.0065 |
| Suprarenal gland    | 0.0000 | Testicles               | 0.0154 |
| Kidney              | 0.0000 | Lung                    | 0.0000 |
| Placenta            | 0.0000 | Nerves                  | 0.0205 |
| Prostate            | 0.0000 | Prostate                | 0.0000 |
| Sensory organs      | 0.0126 | Sensory Organs          | 0.0000 |
|                     |        | Uterus_n                | 0.0167 |

## Electronic Northern for SEQ. ID NO.: 29

|                      | NORMAL      | TUMOR       | Ratios  |        |
|----------------------|-------------|-------------|---------|--------|
|                      | % frequency | % frequency | N/T     | T/N    |
| Bladder              | 0.0312      | 0.0051      | 6.1018  | 0.1639 |
| Breast               | 0.0307      | 0.0019      | 16.3327 | 0.0612 |
| Small intestine      | 0.0061      | 0.0000      | undef   | 0.0000 |
| Ovary                | 0.0120      | 0.0000      | undef   | 0.0000 |
| Endocrine tissue     | 0.0000      | 0.0075      | 0.0000  | undef  |
| Gastrointestinal     | 0.0057      | 0.0093      | 0.6213  | 1.6096 |
| Brain                | 0.0015      | 0.0062      | 0.2400  | 4.1669 |
| Hematopoietic        | 0.0000      | 0.0000      | undef   | undef  |
| Skin                 | 0.0147      | 0.0000      | undef   | 0.0000 |
| Hepatic              | 0.0095      | 0.0065      | 1.4706  | 0.6800 |
| Heart                | 0.0138      | 0.0412      | 0.3341  | 2.9932 |
| Testicles            | 0.0403      | 0.0000      | undef   | 0.0000 |
| Lung                 | 0.0114      | 0.0061      | 1.8628  | 0.5368 |
| Stomach-esophagus    | 0.0193      | 0.0153      | 1.2605  | 0.7933 |
| Muscle-skeleton      | 0.0274      | 0.0300      | 0.9138  | 1.0944 |
| Kidney               | 0.0000      | 0.0000      | undef   | undef  |
| Pancreas             | 0.0050      | 0.0331      | 0.1496  | 6.6857 |
| Penis                | 0.0359      | 0.0000      | undef   | 0.0000 |
| Prostate             | 0.0044      | 0.0021      | 2.0473  | 0.4885 |
| Uterus-endometrium   | 0.0203      | 0.0000      | undef   | 0.0000 |
| Uterus-myometrium    | 0.0686      | 0.0679      | 1.0100  | 0.9901 |
| Uterus-general       | 0.0458      | 0.0000      | undef   | 0.0000 |
| Breast hyperplasia   | 0.0128      |             |         |        |
| Prostate hyperplasia | 0.0119      |             |         |        |
| Seminal vesicle      | 0.0000      |             |         |        |
| Sensory organs       | 0.0118      |             |         |        |
| White blood cells    | 0.0000      |             |         |        |
| Cervix               | 0.0213      |             |         |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |             |
|---------------------|-------------|-------------------------|-------------|
|                     | % frequency | LIBRARIES               | % frequency |
| Development         | 0.0000      | Breast                  | 0.0000      |
| Gastrointestinal    | 0.0111      | Ovary_n                 | 0.0000      |
| Brain               | 0.0000      | Ovary_t                 | 0.0051      |
| Hematopoietic       | 0.0039      | Endocrine tissue        | 0.0000      |
| Skin                | 0.0000      | Fetal                   | 0.0023      |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0122      |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000      |
| Lung                | 0.0036      | Skin-muscle             | 0.0097      |
| Suprarenal gland    | 0.0036      | Testicles               | 0.0077      |
| Kidney              | 0.0000      | Lung                    | 0.0410      |
| Placenta            | 0.0124      | Nerves                  | 0.0010      |
| Prostate            | 0.0061      | Prostate                | 0.0000      |
| Sensory organs      | 0.0249      | Sensory Organs          | 0.0000      |
|                     | 0.0000      | Uterus_n                | 0.0250      |

## Electronic Northern for SEQ. ID NO.: 30

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0273      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0017      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0007      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0027      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0021      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0022      | 0.0021      | 1.0236 | 0.9769 |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      |             |        |        |
| Breast hyperplasia   | 0.0059      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0003      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0056      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0041 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0122 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000 |
| Lung                | 0.0000      | Skin-muscle             | 0.0000 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0000 |
| Placenta            | 0.0000      | Nerves                  | 0.0010 |
| Prostate            | 0.0000      | Prostate                | 0.0000 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0125 |



| Electronic Northern for SEQ. ID NO.: 31 |             |             |        |        |
|---|-------------|-------------|--------|--------|
|   | NORMAL      | TUMOR       | Ratios |        |
|   | % frequency | % frequency | N/T    | T/N    |
| Bladder                                 | 0.0234      | 0.0000      | undef  | 0.0000 |
| Breast                                  | 0.0038      | 0.0000      | undef  | 0.0000 |
| Small intestine                         | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                                   | 0.0000      | 0.0026      | 0.0000 | undef  |
| Endocrine tissue                        | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal                        | 0.0000      | 0.0000      | undef  | undef  |
| Brain                                   | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic                           | 0.0000      | 0.0000      | undef  | undef  |
| Skin                                    | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic                                 | 0.0000      | 0.0000      | undef  | undef  |
| Heart                                   | 0.0053      | 0.0000      | undef  | 0.0000 |
| Testicles                               | 0.0000      | 0.0000      | undef  | undef  |
| Lung                                    | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus                       | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton                         | 0.0069      | 0.0000      | undef  | 0.0000 |
| Kidney                                  | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas                                | 0.0033      | 0.0055      | 0.5983 | 1.6714 |
| Penis                                   | 0.0060      | 0.0000      | undef  | 0.0000 |
| Prostate                                | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium                      | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium                       | 0.0076      | 0.0068      | 1.1223 | 0.8911 |
| Uterus-general                          | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia                      | 0.0000      |             |        |        |
| Prostate hyperplasia                    | 0.0000      |             |        |        |
| Seminal vesicle                         | 0.0000      |             |        |        |
| Sensory organs                          | 0.0000      |             |        |        |
| White blood cells                       | 0.0000      |             |        |        |
| Cervix                                  |             |             |        |        |

| FETUS       | STANDARDIZED/SUBTRACTED |        |
|-------------|-------------------------|--------|
| % frequency | LIBRARIES               |        |
|             | % frequency             |        |
| 0.0000      | Breast                  | 0.0000 |
| 0.0028      | Ovary_n                 | 0.0000 |
| 0.0000      | Ovary_t                 | 0.0000 |
| 0.0000      | Endocrine tissue        | 0.0000 |
| 0.0000      | Fetal                   | 0.0012 |
| 0.0000      | Gastrointestinal        | 0.0000 |
| 0.0107      | Hematopoietic           | 0.0000 |
| 0.0072      | Skin-muscle             | 0.0000 |
| 0.0254      | Testicles               | 0.0000 |
| 0.0000      | Lung                    | 0.0000 |
| 0.0000      | Nerves                  | 0.0000 |
| 0.0499      | Prostate                | 0.0000 |
| 0.0000      | Sensory Organs          | 0.0000 |
|             | Uterus_n                |        |

| Electronic Northern for SEQ. ID NO.: 32 |             |             |        |        |  |
|---|-------------|-------------|--------|--------|--|
|   | NORMAL      | TUMOR       | Ratios |        |  |
|   | % frequency | % frequency | N/T    | T/N    |  |
| Bladder                                 | 0.0234      | 0.0026      | 9.1527 | 0.1093 |  |
| Breast                                  | 0.0000      | 0.0000      | undef  | undef  |  |
| Small intestine                         | 0.0000      | 0.0000      | undef  | undef  |  |
| Ovary                                   | 0.0000      | 0.0026      | 0.0000 | undef  |  |
| Endocrine tissue                        | 0.0000      | 0.0050      | 0.0000 | undef  |  |
| Gastrointestinal                        | 0.0000      | 0.0000      | undef  | undef  |  |
| Brain                                   | 0.0007      | 0.0000      | undef  | 0.0000 |  |
| Hematopoietic                           | 0.0000      | 0.0000      | undef  | undef  |  |
| Skin                                    | 0.0000      | 0.0000      | undef  | undef  |  |
| Hepatic                                 | 0.0000      | 0.0000      | undef  | undef  |  |
| Heart                                   | 0.0000      | 0.0000      | undef  | undef  |  |
| Testicles                               | 0.0000      | 0.0000      | undef  | undef  |  |
| Lung                                    | 0.0000      | 0.0000      | undef  | undef  |  |
| Stomach-esophagus                       | 0.0097      | 0.0000      | undef  | 0.0000 |  |
| Muscle-skeleton                         | 0.0000      | 0.0000      | undef  | undef  |  |
| Kidney                                  | 0.0027      | 0.0000      | undef  | 0.0000 |  |
| Pancreas                                | 0.0000      | 0.0000      | undef  | undef  |  |
| Penis                                   | 0.0000      | 0.0000      | undef  | undef  |  |
| Prostate                                | 0.0000      | 0.0000      | undef  | undef  |  |
| Uterus-endometrium                      | 0.0000      | 0.0000      | undef  | undef  |  |
| Uterus-myometrium                       | 0.0000      | 0.0000      | undef  | undef  |  |
| Uterus-general                          | 0.0000      | 0.0000      | undef  | undef  |  |
| Breast hyperplasia                      | 0.0000      |             |        |        |  |
| Prostate hyperplasia                    | 0.0000      |             |        |        |  |
| Seminal vesicle                         | 0.0000      |             |        |        |  |
| Sensory organs                          | 0.0017      |             |        |        |  |
| White blood cells                       | 0.0000      |             |        |        |  |
| Cervix                                  |             |             |        |        |  |

| FETUS               |             | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0028      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0052 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0036      | Hematopoietic           | 0.0057 |
| Lung                | 0.0000      | Skin-muscle             | 0.0032 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0000 |
| Placenta            | 0.0121      | Nerves                  | 0.0000 |
| Prostate            | 0.0000      | Prostate                | 0.0068 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0077 |
|                     |             | Uterus_n                | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 33

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0195      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0013      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0060      | 0.0104      | 0.5756 | 1.7372 |
| Endocrine tissue     | 0.0085      | 0.0150      | 0.5660 | 1.7667 |
| Gastrointestinal     | 0.0019      | 0.0139      | 0.1391 | 7.2434 |
| Brain                | 0.0037      | 0.0010      | 3.5998 | 0.2778 |
| Hematopoietic        | 0.0040      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0011      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0173      | 0.0117      | 1.4759 | 0.6775 |
| Lung                 | 0.0042      | 0.0061      | 0.6774 | 1.4763 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0060      | 0.0000 | undef  |
| Kidney               | 0.0109      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0017      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0120      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0000      | 0.0021      | 0.0000 | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0076      | 0.0000      | undef  | 0.0000 |
| Uterus-general       | 0.0051      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0026      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0063 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0023 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0036 | Skin-muscle      | 0.0130 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0082 |
| Placenta            | 0.0000 | Nerves           | 0.0070 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0042 |
|                     |        | Uterus_n         |        |

Electronic Northern for SEQ. ID NO.: 34

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0042 |

## Electronic Northern for SEQ. ID NO.: 35

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0013      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0025      | 0.0000 | undef  |
| Gastrointestinal     | 0.0019      | 0.0046      | 0.4142 | 2.4145 |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0011      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0017      | 0.0060      | 0.2856 | 3.5020 |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0035 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0032 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0020 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0310 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0042 |
|                     |        | Uterus_n         |        |

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0195      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      |             |        |        |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS<br>% frequency | STANDARDIZED/SUBTRACTED<br>LIBRARIES<br>% frequency |        |
|---------------------|----------------------|---|--------|
| Development         | 0.0000               | Breast  | 0.0000 |
| Gastrointestinal    | 0.0000               | Ovary_n   | 0.0000 |
| Brain               | 0.0000               | Ovary_t   | 0.0000 |
| Hematopoietic       | 0.0039               | Endocrine tissue                                    | 0.0000 |
| Skin                | 0.0000               | Fetal   | 0.0000 |
| Hepatic             | 0.0000               | Gastrointestinal                                    | 0.0000 |
| Heart-blood vessels | 0.0000               | Hematopoietic                                       | 0.0000 |
| Lung                | 0.0000               | Skin-muscle   | 0.0000 |
| Suprarenal gland    | 0.0000               | Testicles   | 0.0000 |
| Kidney              | 0.0000               | Lung  | 0.0000 |
| Placenta            | 0.0000               | Nerves  | 0.0000 |
| Prostate            | 0.0000               | Prostate  | 0.0000 |
| Sensory organs      | 0.0000               | Sensory Organs                                      | 0.0000 |
|                     |                      | Uterus_n  | 0.0000 |

Electronic Northern for SEQ. ID NO.: 37

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0038      | 0.0038      | 1.0208 | 0.9796 |
| Small intestine      | 0.0184      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0090      | 0.0052      | 1.7269 | 0.5791 |
| Endocrine tissue     | 0.0068      | 0.0025      | 2.7170 | 0.3681 |
| Gastrointestinal     | 0.0057      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0089      | 0.0144      | 0.6171 | 1.6205 |
| Hematopoietic        | 0.0040      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0095      | 0.0065      | 1.4706 | 0.6800 |
| Heart                | 0.0095      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0115      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0135      | 0.0123      | 1.1007 | 0.9085 |
| Stomach-esophagus    | 0.0097      | 0.0077      | 1.2605 | 0.7933 |
| Muscle-skeleton      | 0.0034      | 0.0120      | 0.2856 | 3.5020 |
| Kidney               | 0.0054      | 0.0068      | 0.7930 | 1.2610 |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0060      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0022      | 0.0149      | 0.1462 | 6.8384 |
| Uterus-endometrium   | 0.0135      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0076      | 0.0136      | 0.5611 | 1.7821 |
| Uterus-general       | 0.0255      | 0.1908      | 0.1334 | 7.4943 |
| Breast hyperplasia   | 0.0096      |             |        |        |
| Prostate hyperplasia | 0.0059      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0118      |             |        |        |
| White blood cells    | 0.0104      |             |        |        |
| Cervix               | 0.0000      |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0056 | Ovary_n          | 0.1595 |
| Brain               | 0.0000 | Ovary_t          | 0.0253 |
| Hematopoietic       | 0.0118 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0116 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0366 |
| Heart-blood vessels | 0.0036 | Hematopoietic    | 0.0456 |
| Lung                | 0.0108 | Skin-muscle      | 0.0162 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0062 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0221 |
| Prostate            | 0.0000 | Prostate         | 0.0068 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0077 |
|                     |        | Uterus_n         | 0.0000 |

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0273      | 0.0051      | 5.3391 | 0.1873 |
| Breast               | 0.0026      | 0.0075      | 0.3403 | 2.9389 |
| Small intestine      | 0.0061      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0068      | 0.0125      | 0.5434 | 1.8403 |
| Gastrointestinal     | 0.0019      | 0.0046      | 0.4142 | 2.4145 |
| Brain                | 0.0081      | 0.0031      | 2.6399 | 0.3788 |
| Hematopoietic        | 0.0040      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0257      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0048      | 0.0000      | undef  | 0.0000 |
| Heart                | 0.0064      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0042      | 0.0102      | 0.4064 | 2.4605 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0069      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0136      | 0.0205      | 0.6609 | 1.5132 |
| Pancreas             | 0.0033      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0090      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0109      | 0.0021      | 5.1181 | 0.1954 |
| Uterus-endometrium   | 0.0068      | 0.0528      | 0.1280 | 7.8106 |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0128      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      | 0.0000      | undef  | undef  |
| Prostate hyperplasia | 0.0089      | 0.0000      | undef  | undef  |
| Seminal vesicle      | 0.0235      | 0.0000      | undef  | undef  |
| Sensory organs       | 0.0009      | 0.0000      | undef  | undef  |
| White blood cells    | 0.0000      | 0.0000      | undef  | undef  |
| Cervix               | 0.0000      | 0.0000      | undef  | undef  |

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0056 | Ovary_n          | 0.0000 |
| Brain               | 0.0125 | Ovary_t          | 0.0051 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0012 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0107 | Hematopoietic    | 0.0000 |
| Lung                | 0.0036 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0507 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0164 |
| Placenta            | 0.0000 | Nerves           | 0.0070 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |



## Electronic Northern for SEQ. ID NO.: 39

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0195      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0017      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0020      | 0.0000 | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

| FETUS               |        | STANDARDIZED/SUBTRACTED |        |
|---------------------|--------|-------------------------|--------|
| % frequency         |        | LIBRARIES               |        |
|                     |        | % frequency             |        |
| Development         | 0.0000 | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n                 | 0.0000 |
| Brain               | 0.0000 | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000 | Fetal                   | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic           | 0.0000 |
| Lung                | 0.0000 | Skin-muscle             | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles               | 0.0000 |
| Kidney              | 0.0000 | Lung                    | 0.0000 |
| Placenta            | 0.0000 | Nerves                  | 0.0000 |
| Prostate            | 0.0000 | Prostate                | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs          | 0.0000 |
|                     |        | Uterus_n                |        |

## Electronic Northern for SEQ. ID NO.: 40

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0156                | 0.0000               | undef         | 0.0000 |
| Breast               | 0.0013                | 0.0019               | 0.6805        | 1.4694 |
| Small intestine      | 0.0031                | 0.0000               | undef         | 0.0000 |
| Ovary                | 0.0000                | 0.0026               | 0.0000        | undef  |
| Endocrine tissue     | 0.0034                | 0.0050               | 0.6792        | 1.4722 |
| Gastrointestinal     | 0.0057                | 0.0000               | undef         | 0.0000 |
| Brain                | 0.0007                | 0.0031               | 0.2400        | 4.1669 |
| Hematopoietic        | 0.0040                | 0.0000               | undef         | 0.0000 |
| Skin                 | 0.0000                | 0.0000               | undef         | undef  |
| Hepatic              | 0.0000                | 0.0000               | undef         | undef  |
| Heart                | 0.0058                | 0.0000               | undef         | 0.0000 |
| Testicles            | 0.0021                | 0.0041               | 0.5080        | 1.9684 |
| Lung                 | 0.0000                | 0.0000               | undef         | undef  |
| Stomach-esophagus    | 0.0086                | 0.0000               | undef         | 0.0000 |
| Muscle-skeleton      | 0.0027                | 0.0000               | undef         | 0.0000 |
| Kidney               | 0.0033                | 0.0000               | undef         | 0.0000 |
| Pancreas             | 0.0000                | 0.0000               | undef         | undef  |
| Penis                | 0.0000                | 0.0000               | undef         | undef  |
| Prostate             | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-endometrium   | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-myometrium    | 0.0051                | 0.0000               | undef         | 0.0000 |
| Uterus-general       | 0.0032                |                      |               |        |
| Breast hyperplasia   | 0.0000                |                      |               |        |
| Prostate hyperplasia | 0.0000                |                      |               |        |
| Seminal vesicle      | 0.0000                |                      |               |        |
| Sensory organs       | 0.0000                |                      |               |        |
| White blood cells    | 0.0000                |                      |               |        |
| Cervix               |                       |                      |               |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0136 |
| Gastrointestinal    | 0.0056 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0035 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic    | 0.0000 |
| Lung                | 0.0072 | Skin-muscle      | 0.0227 |
| Suprarenal gland    | 0.0254 | Testicles        | 0.0077 |
| Kidney              | 0.0062 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0050 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0077 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 43

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0026      | 0.0019      | 1.3611 | 0.7347 |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0000      | 0.0026      | 0.0000 | undef  |
| Endocrine tissue     | 0.0017      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0019      | 0.0093      | 0.2071 | 4.8299 |
| Brain                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0032      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0052      | 0.0041      | 1.2701 | 0.7973 |
| Stomach-esophagus    | 0.0193      | 0.0000      | undef  | 0.0000 |
| Muscle-skeleton      | 0.0069      | 0.0060      | 1.1422 | 0.8755 |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0017      | 0.0055      | 0.2931 | 3.3428 |
| Penis                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0000      | 0.0021      | 0.0000 | undef  |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0000      | 0.0068      | 0.0000 | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0032      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0118      |             |        |        |
| Sensory organs       | 0.0017      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0152 |
| Hematopoietic       | 0.0039 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0244 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0071 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0036 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0010 |
| Prostate            | 0.0000 | Prostate         | 0.0068 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0042 |

## Electronic Northern for SEQ. ID NO.: 44

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0195      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      |             |        |        |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 46

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      |             |        |        |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

Electronic Northern for SEQ. ID NO.: 47

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0273      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0010      | 0.0000 | undef  |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0010      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0009      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 48

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0273      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0013      | 0.0019      | 0.6805 | 1.4694 |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0030      | 0.0052      | 0.5756 | 1.7372 |
| Endocrine tissue     | 0.0017      | 0.0025      | 0.6792 | 1.4722 |
| Gastrointestinal     | 0.0019      | 0.0046      | 0.4142 | 2.4145 |
| Brain                | 0.0007      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0048      | 0.0000      | undef  | 0.0000 |
| Heart                | 0.0042      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0010      | 0.0020      | 0.5080 | 1.9684 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0034      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0022      | 0.0021      | 1.0236 | 0.9769 |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0000      | 0.0068      | 0.0000 | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0064      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0017      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0278 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0017 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic    | 0.0000 |
| Lung                | 0.0072 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0060 |
| Placenta            | 0.0061 | Nerves           | 0.0000 |
| Prostate            | 0.0249 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 50

|                      | NORMAL      | TUMOR       | Ratio |        |
|----------------------|-------------|-------------|-------|--------|
|                      | % frequency | % frequency | N/T   | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef | undef  |
| Ovary                | 0.0000      | 0.0000      | undef | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef | undef  |
| Brain                | 0.0000      | 0.0000      | undef | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef | undef  |
| Skin                 | 0.0000      | 0.0000      | undef | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef | undef  |
| Heart                | 0.0000      | 0.0000      | undef | undef  |
| Testicles            | 0.0000      | 0.0000      | undef | undef  |
| Lung                 | 0.0000      | 0.0000      | undef | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef | undef  |
| Kidney               | 0.0000      | 0.0000      | undef | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef | undef  |
| Penis                | 0.0000      | 0.0000      | undef | undef  |
| Prostate             | 0.0000      | 0.0000      | undef | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef | undef  |
| Uterus-general       | 0.0000      |             |       |        |
| Breast hyperplasia   | 0.0000      |             |       |        |
| Prostate hyperplasia | 0.0000      |             |       |        |
| Seminal vesicle      | 0.0000      |             |       |        |
| Sensory organs       | 0.0000      |             |       |        |
| White blood cells    | 0.0000      |             |       |        |
| Cervix               |             |             |       |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |



Electronic Northern for SEQ. ID NO.: 51  
 NORMAL TUMOR Ratios  
 % frequency % frequency N/T T/N

|                      |        |        |        |        |
|----------------------|--------|--------|--------|--------|
| Bladder              | 0.0156 | 0.0000 | undef  | 0.0000 |
| Breast               | 0.0026 | 0.0000 | undef  | 0.0000 |
| Small intestine      | 0.0000 | 0.0000 | undef  | undef  |
| Ovary                | 0.0060 | 0.0078 | 0.7675 | 1.3029 |
| Endocrine tissue     | 0.0034 | 0.0025 | 1.3585 | 0.7361 |
| Gastrointestinal     | 0.0057 | 0.0000 | undef  | 0.0000 |
| Brain                | 0.0022 | 0.0021 | 1.0799 | 0.9260 |
| Hematopoietic        | 0.0027 | 0.0000 | undef  | 0.0000 |
| Skin                 | 0.0000 | 0.0000 | undef  | undef  |
| Hepatic              | 0.0000 | 0.0000 | undef  | undef  |
| Heart                | 0.0053 | 0.0000 | undef  | 0.0000 |
| Testicles            | 0.0000 | 0.0000 | undef  | undef  |
| Lung                 | 0.0031 | 0.0000 | undef  | 0.0000 |
| Stomach-esophagus    | 0.0000 | 0.0000 | undef  | undef  |
| Muscle-skeleton      | 0.0000 | 0.0000 | undef  | undef  |
| Kidney               | 0.0000 | 0.0165 | 0.0000 | undef  |
| Pancreas             | 0.0000 | 0.0000 | undef  | undef  |
| Penis                | 0.0022 | 0.0000 | undef  | 0.0000 |
| Prostate             | 0.0068 | 0.0000 | undef  | 0.0000 |
| Uterus-endometrium   | 0.0000 | 0.0000 | undef  | undef  |
| Uterus-myometrium    | 0.0000 | 0.0000 | undef  | undef  |
| Uterus-general       | 0.0032 |        |        |        |
| Breast hyperplasia   | 0.0059 |        |        |        |
| Prostate hyperplasia | 0.0000 |        |        |        |
| Seminal vesicle      | 0.0000 |        |        |        |
| Sensory organs       | 0.0026 |        |        |        |
| White blood cells    | 0.0000 |        |        |        |
| Cervix               |        |        |        |        |

FETUS  
 % frequency

STANDARDIZED/SUBTRACTED  
 LIBRARIES  
 % frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0136 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0041 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0057 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0061 | Nerves           | 0.0068 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 52

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0312      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0010      | 0.0000 | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      | 0.0000      | undef  | undef  |
| Prostate hyperplasia | 0.0000      | 0.0000      | undef  | undef  |
| Seminal vesicle      | 0.0000      | 0.0000      | undef  | undef  |
| Sensory organs       | 0.0000      | 0.0000      | undef  | undef  |
| White blood cells    | 0.0000      | 0.0000      | undef  | undef  |
| Cervix               | 0.0000      | 0.0000      | undef  | undef  |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 53

|                      | NORMAL      | TUMOR       | Ratio  |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0195      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0010      | 0.0000 | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0011      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0027      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0000      | 0.0055      | 0.0000 | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0076      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      |             |        |        |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0028 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0039 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0032 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0020 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

Electronic Northern for SEQ. ID NO.: 54

|  | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratio<br>N/T | T/N |
|--|-----------------------|----------------------|--------------|-----|
|--|-----------------------|----------------------|--------------|-----|

|                      |        |        |        |        |
|----------------------|--------|--------|--------|--------|
| Bladder              | 0.0195 | 0.0000 | undef  | 0.0000 |
| Breast               | 0.0000 | 0.0000 | undef  | undef  |
| Small intestine      | 0.0000 | 0.0000 | undef  | undef  |
| Ovary                | 0.0000 | 0.0000 | undef  | undef  |
| Endocrine tissue     | 0.0000 | 0.0000 | undef  | undef  |
| Gastrointestinal     | 0.0000 | 0.0093 | 0.0000 | undef  |
| Brain                | 0.0000 | 0.0010 | 0.0000 | undef  |
| Hematopoietic        | 0.0000 | 0.0000 | undef  | undef  |
| Skin                 | 0.0000 | 0.0000 | undef  | undef  |
| Hepatic              | 0.0000 | 0.0000 | undef  | undef  |
| Heart                | 0.0000 | 0.0000 | undef  | undef  |
| Testicles            | 0.0000 | 0.0020 | 0.0000 | undef  |
| Lung                 | 0.0000 | 0.0000 | undef  | undef  |
| Stomach-esophagus    | 0.0000 | 0.0000 | undef  | undef  |
| Muscle-skeleton      | 0.0000 | 0.0000 | undef  | undef  |
| Kidney               | 0.0000 | 0.0055 | 0.0000 | undef  |
| Pancreas             | 0.0000 | 0.0000 | undef  | undef  |
| Penis                | 0.0000 | 0.0000 | undef  | undef  |
| Prostate             | 0.0000 | 0.0000 | undef  | undef  |
| Uterus-endometrium   | 0.0076 | 0.0000 | undef  | 0.0000 |
| Uterus-myometrium    | 0.0000 | 0.0000 | undef  | undef  |
| Uterus-general       | 0.0064 |        |        |        |
| Breast hyperplasia   | 0.0000 |        |        |        |
| Prostate hyperplasia | 0.0000 |        |        |        |
| Seminal vesicle      | 0.0000 |        |        |        |
| Sensory organs       | 0.0000 |        |        |        |
| White blood cells    | 0.0106 |        |        |        |
| Cervix               |        |        |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0037 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 55

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0234                | 0.0000               | undef         | 0.0000 |
| Breast               | 0.0000                | 0.0000               | undef         | undef  |
| Small intestine      | 0.0000                | 0.0000               | undef         | undef  |
| Ovary                | 0.0000                | 0.0000               | undef         | undef  |
| Endocrine tissue     | 0.0000                | 0.0000               | undef         | undef  |
| Gastrointestinal     | 0.0000                | 0.0000               | undef         | undef  |
| Brain                | 0.0000                | 0.0000               | undef         | undef  |
| Hematopoietic        | 0.0013                | 0.0000               | undef         | 0.0000 |
| Skin                 | 0.0000                | 0.0000               | undef         | undef  |
| Hepatic              | 0.0000                | 0.0000               | undef         | undef  |
| Heart                | 0.0000                | 0.0000               | undef         | undef  |
| Testicles            | 0.0000                | 0.0000               | undef         | undef  |
| Lung                 | 0.0000                | 0.0000               | undef         | undef  |
| Stomach-esophagus    | 0.0000                | 0.0077               | 0.0000        | undef  |
| Muscle-skeleton      | 0.0000                | 0.0000               | undef         | undef  |
| Kidney               | 0.0000                | 0.0000               | undef         | undef  |
| Pancreas             | 0.0000                | 0.0000               | undef         | undef  |
| Penis                | 0.0000                | 0.0000               | undef         | undef  |
| Prostate             | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-endometrium   | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-myometrium    | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-general       | 0.0000                | 0.0000               | undef         | undef  |
| Breast hyperplasia   | 0.0000                |                      |               |        |
| Prostate hyperplasia | 0.0000                |                      |               |        |
| Seminal vesicle      | 0.0000                |                      |               |        |
| Sensory organs       | 0.0000                |                      |               |        |
| White blood cells    | 0.0000                |                      |               |        |
| Cervix               |                       |                      |               |        |

| FETUS<br>% frequency | STANDARDIZED/SUBTRACTED<br>LIBRARIES<br>% frequency |        |
|----------------------|---|--------|
| Development          | Breast  | 0.0000 |
| Gastrointestinal     | Ovary_n   | 0.0000 |
| Brain                | Ovary_t   | 0.0000 |
| Hematopoietic        | Endocrine tissue                                    | 0.0000 |
| Skin                 | Fetal   | 0.0000 |
| Hepatic              | Gastrointestinal                                    | 0.0000 |
| Heart-blood vessels  | Hematopoietic                                       | 0.0000 |
| Lung                 | Skin-muscle   | 0.0000 |
| Suprarenal gland     | Testicles   | 0.0000 |
| Kidney               | Lung  | 0.0000 |
| Placenta             | Nerves  | 0.0000 |
| Prostate             | Prostate  | 0.0000 |
| Sensory organs       | Sensory Organs                                      | 0.0000 |
|                      | Uterus_n  |        |

Electronic Northern for SEQ. ID NO.: 56

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0026      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0051      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0038      | 0.0093      | 0.4142 | 2.4145 |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0011      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0010      | 0.0020      | 0.5080 | 1.9684 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0017      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0054      | 0.0068      | 0.7930 | 1.2610 |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0022      | 0.0043      | 0.5118 | 1.9538 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0030      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0009      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

| FETUS               |        | STANDARDIZED/SUBTRACTED |        |
|---------------------|--------|-------------------------|--------|
| % frequency         |        | LIBRARIES               |        |
|                     |        | % frequency             |        |
| Development         | 0.0000 | Breast                  | 0.0136 |
| Gastrointestinal    | 0.0028 | Ovary_n                 | 0.0000 |
| Brain               | 0.0000 | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000 | Fetal                   | 0.0012 |
| Hepatic             | 0.0000 | Gastrointestinal        | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic           | 0.0228 |
| Lung                | 0.0000 | Skin-muscle             | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles               | 0.0000 |
| Kidney              | 0.0000 | Lung                    | 0.0082 |
| Placenta            | 0.0000 | Nerves                  | 0.0040 |
| Prostate            | 0.0000 | Prostate                | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs          | 0.0000 |
|                     |        | Uterus_n                | 0.0083 |

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0025      | 0.0000 | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0007      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0027      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0010      | 0.0041      | 0.2540 | 3.9367 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0000      | 0.0055      | 0.0000 | undef  |
| Penis                | 0.0000      | 0.0267      | 0.0000 | undef  |
| Prostate             | 0.0065      | 0.0000      | undef  | 0.0000 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0058      | 0.0000 | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0030      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS<br>% frequency | STANDARDIZED/SUBTRACTED<br>LIBRARIES<br>% frequency |        |
|---------------------|----------------------|---|--------|
| Development         | 0.0000               | Breast  | 0.0000 |
| Gastrointestinal    | 0.0000               | Ovary_n   | 0.0000 |
| Brain               | 0.0000               | Ovary_t   | 0.0000 |
| Hematopoietic       | 0.0039               | Endocrine tissue                                    | 0.0000 |
| Skin                | 0.0000               | Fetal   | 0.0000 |
| Hepatic             | 0.0000               | Gastrointestinal                                    | 0.0000 |
| Heart-blood vessels | 0.0036               | Hematopoietic                                       | 0.0000 |
| Lung                | 0.0036               | Skin-muscle   | 0.0000 |
| Suprarenal gland    | 0.0000               | Testicles   | 0.0077 |
| Kidney              | 0.0000               | Lung  | 0.0000 |
| Placenta            | 0.0000               | Nerves  | 0.0000 |
| Prostate            | 0.0000               | Prostate  | 0.0000 |
| Sensory organs      | 0.0000               | Sensory Organs                                      | 0.0000 |
|                     |                      | Uterus_n  | 0.0000 |

Electronic Northern for SEQ. ID NO.: 58  
 NORMAL TUMOR Ratios  
 % frequency % frequency N/T T/N

|                      |        |        |        |        |
|----------------------|--------|--------|--------|--------|
| Bladder              | 0.0234 | 0.0026 | 9.1527 | 0.1093 |
| Breast               | 0.0000 | 0.0000 | undef  | undef  |
| Small intestine      | 0.0000 | 0.0000 | undef  | undef  |
| Ovary                | 0.0000 | 0.0000 | undef  | undef  |
| Endocrine tissue     | 0.0000 | 0.0000 | undef  | undef  |
| Gastrointestinal     | 0.0000 | 0.0000 | undef  | undef  |
| Brain                | 0.0000 | 0.0000 | undef  | undef  |
| Hematopoietic        | 0.0000 | 0.0000 | undef  | undef  |
| Skin                 | 0.0000 | 0.0000 | undef  | undef  |
| Hepatic              | 0.0000 | 0.0000 | undef  | undef  |
| Heart                | 0.0000 | 0.0000 | undef  | undef  |
| Testicles            | 0.0000 | 0.0000 | undef  | undef  |
| Lung                 | 0.0000 | 0.0000 | undef  | undef  |
| Stomach-esophagus    | 0.0000 | 0.0000 | undef  | undef  |
| Muscle-skeleton      | 0.0000 | 0.0000 | undef  | undef  |
| Kidney               | 0.0000 | 0.0000 | undef  | undef  |
| Pancreas             | 0.0000 | 0.0000 | undef  | undef  |
| Penis                | 0.0000 | 0.0000 | undef  | undef  |
| Prostate             | 0.0000 | 0.0000 | undef  | undef  |
| Uterus-endometrium   | 0.0000 | 0.0000 | undef  | undef  |
| Uterus-myometrium    | 0.0000 | 0.0000 | undef  | undef  |
| Uterus-general       | 0.0000 |        |        |        |
| Breast hyperplasia   | 0.0000 |        |        |        |
| Prostate hyperplasia | 0.0000 |        |        |        |
| Seminal vesicle      | 0.0000 |        |        |        |
| Sensory organs       | 0.0000 |        |        |        |
| White blood cells    | 0.0000 |        |        |        |
| Cervix               |        |        |        |        |

FETUS  
 % frequency

STANDARDIZED/SUBTRACTED  
 LIBRARIES  
 % frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |



## Electronic Northern for SEQ. ID NO.: 59

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T T/N |        |
|----------------------|-----------------------|----------------------|-------------------|--------|
| Bladder              | 0.0273                | 0.0000               | undef             | 0.0000 |
| Breast               | 0.0000                | 0.0000               | undef             | undef  |
| Small intestine      | 0.0000                | 0.0000               | undef             | undef  |
| Ovary                | 0.0000                | 0.0000               | undef             | undef  |
| Endocrine tissue     | 0.0000                | 0.0000               | undef             | undef  |
| Gastrointestinal     | 0.0000                | 0.0000               | undef             | undef  |
| Brain                | 0.0000                | 0.0000               | undef             | undef  |
| Hematopoietic        | 0.0000                | 0.0000               | undef             | undef  |
| Skin                 | 0.0000                | 0.0000               | undef             | undef  |
| Hepatic              | 0.0000                | 0.0000               | undef             | undef  |
| Heart                | 0.0000                | 0.0117               | 0.0000            | undef  |
| Testicles            | 0.0000                | 0.0020               | 0.0000            | undef  |
| Lung                 | 0.0000                | 0.0000               | undef             | undef  |
| Stomach-esophagus    | 0.0000                | 0.0000               | undef             | undef  |
| Muscle-skeleton      | 0.0000                | 0.0000               | undef             | undef  |
| Kidney               | 0.0000                | 0.0000               | undef             | undef  |
| Pancreas             | 0.0000                | 0.0000               | undef             | undef  |
| Penis                | 0.0000                | 0.0000               | undef             | undef  |
| Prostate             | 0.0000                | 0.0000               | undef             | undef  |
| Uterus-endometrium   | 0.0000                | 0.0000               | undef             | undef  |
| Uterus-myometrium    | 0.0000                | 0.0000               | undef             | undef  |
| Uterus-general       | 0.0000                |                      |                   |        |
| Breast hyperplasia   | 0.0000                |                      |                   |        |
| Prostate hyperplasia | 0.0000                |                      |                   |        |
| Seminal vesicle      | 0.0000                |                      |                   |        |
| Sensory organs       | 0.0000                |                      |                   |        |
| White blood cells    | 0.0000                |                      |                   |        |
| Cervix               |                       |                      |                   |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0028 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 60

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0051      | 0.0038      | 1.3611 | 0.7347 |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0051      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0038      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0022      | 0.0021      | 1.0799 | 0.9260 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0021      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0060      | 0.0000 | undef  |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0050      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0021      | 0.0000 | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0051      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0032      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0009      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.1595 |
| Brain               | 0.0000 | Ovary_t          | 0.0203 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0070 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 61

|                      | NORMAL      | TUMOR       | Ratios        | T/N |
|----------------------|-------------|-------------|---------------|-----|
|                      | % frequency | % frequency | N/T           |     |
| Bladder              | 0.0156      | 0.0000      | undef 0.0000  |     |
| Breast               | 0.0000      | 0.0000      | undef undef   |     |
| Small intestine      | 0.0061      | 0.0165      | 0.3707 2.6973 |     |
| Ovary                | 0.0030      | 0.0052      | 0.5756 1.7372 |     |
| Endocrine tissue     | 0.0034      | 0.0075      | 0.4528 2.2083 |     |
| Gastrointestinal     | 0.0000      | 0.0046      | 0.0000 undef  |     |
| Brain                | 0.0067      | 0.0051      | 1.2959 0.7716 |     |
| Hematopoietic        | 0.0000      | 0.0000      | undef undef   |     |
| Skin                 | 0.0000      | 0.0000      | undef undef   |     |
| Hepatic              | 0.0000      | 0.0000      | undef undef   |     |
| Heart                | 0.0074      | 0.0000      | undef 0.0000  |     |
| Testicles            | 0.0000      | 0.0117      | 0.0000 undef  |     |
| Lung                 | 0.0031      | 0.0061      | 0.5080 1.9684 |     |
| Stomach-esophagus    | 0.0097      | 0.0077      | 1.2605 0.7933 |     |
| Muscle-skeleton      | 0.0034      | 0.0120      | 0.2856 3.5020 |     |
| Kidney               | 0.0081      | 0.0068      | 1.1896 0.8406 |     |
| Pancreas             | 0.0066      | 0.0000      | undef 0.0000  |     |
| Penis                | 0.0060      | 0.0000      | undef 0.0000  |     |
| Prostate             | 0.0000      | 0.0000      | undef undef   |     |
| Uterus-endometrium   | 0.0000      | 0.0068      | 0.0000 undef  |     |
| Uterus-myometrium    | 0.0153      | 0.0000      | undef 0.0000  |     |
| Uterus-general       | 0.0000      |             |               |     |
| Breast hyperplasia   | 0.0030      |             |               |     |
| Prostate hyperplasia | 0.0000      |             |               |     |
| Seminal vesicle      | 0.0000      |             |               |     |
| Sensory organs       | 0.0061      |             |               |     |
| White blood cells    | 0.0000      |             |               |     |
| Cervix               |             |             |               |     |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0056 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0152 |
| Hematopoietic       | 0.0079 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0064 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0036 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0130 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0082 |
| Placenta            | 0.0000 | Nerves           | 0.0010 |
| Prostate            | 0.0249 | Prostate         | 0.0068 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0042 |

Electronic Northern for SEQ. ID NO.: 62

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0061      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0019      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0022      | 0.0010      | 2.1599 | 0.4630 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0017      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0043      | 0.0000 | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0068 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0063 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0006 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0068 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 63

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0351      | 0.0051      | 6.8645 | 0.1457 |
| Breast               | 0.0026      | 0.0075      | 0.3403 | 2.9389 |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0000      | 0.0052      | 0.0000 | undef  |
| Endocrine tissue     | 0.0034      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0019      | 0.0046      | 0.4142 | 2.4145 |
| Brain                | 0.0015      | 0.0041      | 0.3600 | 2.7779 |
| Hematopoietic        | 0.0027      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0048      | 0.0000      | undef  | 0.0000 |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0058      | 0.0117      | 0.4920 | 2.0326 |
| Lung                 | 0.0042      | 0.0041      | 1.0161 | 0.9842 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0120      | 0.0000 | undef  |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0017      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0022      | 0.0000      | undef  | 0.0000 |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0076      | 0.0000      | undef  | 0.0000 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0089      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0118      |             |        |        |
| Sensory organs       | 0.0009      |             |        |        |
| White blood cells    | 0.0106      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0278 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0012 |
| Skin                | 0.0000 | Fetal            | 0.0122 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0097 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0050 |
| Placenta            | 0.0061 | Nerves           | 0.0068 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0042 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 65

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0195                | 0.0000               | undef         | 0.0000 |
| Breast               | 0.0000                | 0.0000               | undef         | undef  |
| Small intestine      | 0.0000                | 0.0000               | undef         | undef  |
| Ovary                | 0.0000                | 0.0000               | undef         | undef  |
| Endocrine tissue     | 0.0000                | 0.0000               | undef         | undef  |
| Gastrointestinal     | 0.0000                | 0.0000               | undef         | undef  |
| Brain                | 0.0000                | 0.0000               | undef         | undef  |
| Hematopoietic        | 0.0000                | 0.0000               | undef         | undef  |
| Skin                 | 0.0000                | 0.0000               | undef         | undef  |
| Hepatic              | 0.0000                | 0.0000               | undef         | undef  |
| Heart                | 0.0000                | 0.0000               | undef         | undef  |
| Testicles            | 0.0000                | 0.0000               | undef         | undef  |
| Lung                 | 0.0000                | 0.0000               | undef         | undef  |
| Stomach-esophagus    | 0.0000                | 0.0000               | undef         | undef  |
| Muscle-skeleton      | 0.0000                | 0.0000               | 0.0000        | undef  |
| Kidney               | 0.0000                | 0.0000               | undef         | undef  |
| Pancreas             | 0.0000                | 0.0000               | undef         | undef  |
| Penis                | 0.0030                | 0.0000               | undef         | 0.0000 |
| Prostate             | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-endometrium   | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-myometrium    | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-general       | 0.0000                | 0.0000               | undef         | undef  |
| Breast hyperplasia   | 0.0000                |                      |               |        |
| Prostate hyperplasia | 0.0089                |                      |               |        |
| Seminal vesicle      | 0.0000                |                      |               |        |
| Sensory organs       | 0.0000                |                      |               |        |
| White blood cells    | 0.0000                |                      |               |        |
| Cervix               |                       |                      |               |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0077 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

Electronic Northern for SEQ. ID NO.: 67

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0390      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0017      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0235      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           |        |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0245 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0037 |
| Lung                | 0.0036 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 69

|                      | NORMAL      | TUMOR       | Ratios  | T/N     |
|----------------------|-------------|-------------|---------|---------|
|                      | % frequency | % frequency | N/T     |         |
| Bladder              | 0.0858      | 0.0077      | 11.1866 | 0.0894  |
| Breast               | 0.0102      | 0.0075      | 1.3611  | 0.7347  |
| Small intestine      | 0.0092      | 0.0000      | undef   | 0.0000  |
| Ovary                | 0.0060      | 0.0260      | 0.2303  | 4.3431  |
| Endocrine tissue     | 0.0068      | 0.0125      | 0.5434  | 1.8403  |
| Gastrointestinal     | 0.0038      | 0.0278      | 0.1381  | 7.2434  |
| Brain                | 0.0022      | 0.0144      | 0.1543  | 6.4818  |
| Hematopoietic        | 0.0013      | 0.0379      | 0.0353  | 28.3379 |
| Skin                 | 0.0734      | 0.1695      | 0.4332  | 2.3084  |
| Hepatic              | 0.0000      | 0.0194      | 0.0000  | undef   |
| Heart                | 0.0159      | 0.0137      | 1.1565  | 0.8647  |
| Testicles            | 0.0000      | 0.0468      | 0.0000  | undef   |
| Lung                 | 0.0073      | 0.0164      | 0.4445  | 2.2496  |
| Stomach-esophagus    | 0.0000      | 0.0230      | 0.0000  | undef   |
| Muscle-skeleton      | 0.0069      | 0.0180      | 0.3807  | 2.6265  |
| Kidney               | 0.0163      | 0.0000      | undef   | 0.0000  |
| Pancreas             | 0.0066      | 0.0055      | 1.1966  | 0.8357  |
| Penis                | 0.0210      | 0.0267      | 0.7862  | 1.2719  |
| Prostate             | 0.0044      | 0.0021      | 2.0473  | 0.4885  |
| Uterus-endometrium   | 0.0338      | 0.0000      | undef   | 0.0000  |
| Uterus-myometrium    | 0.0076      | 0.0068      | 1.1223  | 0.8911  |
| Uterus-general       | 0.0255      | 0.0000      | undef   | 0.0000  |
| Breast hyperplasia   | 0.0128      |             |         |         |
| Prostate hyperplasia | 0.0119      |             |         |         |
| Seminal vesicle      | 0.0000      |             |         |         |
| Sensory organs       | 0.0235      |             |         |         |
| White blood cells    | 0.0000      |             |         |         |
| Cervix               | 0.0000      |             |         |         |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0139 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0028 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0051 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0245 |
| Skin                | 0.0000 | Fetal            | 0.0128 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0462 | Hematopoietic    | 0.0000 |
| Lung                | 0.0036 | Skin-muscle      | 0.0227 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0154 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0171 |
| Prostate            | 0.0000 | Prostate         | 0.0068 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0155 |
|                     |        | Uterus_n         | 0.0000 |



## Electronic Northern for SEQ. ID NO.: 72

|  | NORMAL      | TUMOR       | Ratios |     |
|--|-------------|-------------|--------|-----|
|  | % frequency | % frequency | N/T    | T/N |

|                      |        |        |         |        |
|----------------------|--------|--------|---------|--------|
| Bladder              | 0.0585 | 0.0077 | 7.6272  | 0.1311 |
| Breast               | 0.0192 | 0.0019 | 10.2079 | 0.0980 |
| Small intestine      | 0.0123 | 0.0000 | undef   | 0.0000 |
| Ovary                | 0.0090 | 0.0052 | 1.7269  | 0.5791 |
| Endocrine tissue     | 0.0000 | 0.0075 | 0.0000  | undef  |
| Gastrointestinal     | 0.0307 | 0.0000 | undef   | 0.0000 |
| Brain                | 0.0118 | 0.0062 | 1.9199  | 0.5209 |
| Hematopoietic        | 0.0013 | 0.0000 | undef   | 0.0000 |
| Skin                 | 0.0184 | 0.0000 | undef   | 0.0000 |
| Hepatic              | 0.0190 | 0.0065 | 2.9412  | 0.3400 |
| Heart                | 0.0244 | 0.0000 | undef   | 0.0000 |
| Testicles            | 0.0058 | 0.0000 | undef   | 0.0000 |
| Lung                 | 0.0010 | 0.0041 | 0.2540  | 3.9367 |
| Stomach-esophagus    | 0.0000 | 0.0077 | 0.0000  | undef  |
| Muscle-skeleton      | 0.0086 | 0.0000 | undef   | 0.0000 |
| Kidney               | 0.0054 | 0.0000 | undef   | 0.0000 |
| Pancreas             | 0.0033 | 0.0000 | undef   | 0.0000 |
| Penis                | 0.0509 | 0.0000 | undef   | 0.0000 |
| Prostate             | 0.0153 | 0.0085 | 1.7913  | 0.5582 |
| Uterus-endometrium   | 0.0135 | 0.0000 | undef   | 0.0000 |
| Uterus-myometrium    | 0.0152 | 0.0000 | undef   | 0.0000 |
| Uterus-general       | 0.0102 | 0.0000 | undef   | 0.0000 |
| Breast hyperplasia   | 0.0320 |        |         |        |
| Prostate hyperplasia | 0.0238 |        |         |        |
| Seminal vesicle      | 0.0089 |        |         |        |
| Sensory organs       | 0.0000 |        |         |        |
| White blood cells    | 0.0000 |        |         |        |
| Cervix               | 0.0000 |        |         |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0204 |
| Gastrointestinal    | 0.0167 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0101 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0082 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0071 | Hematopoietic    | 0.0162 |
| Lung                | 0.0036 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0082 |
| Kidney              | 0.0000 | Lung             | 0.0040 |
| Placenta            | 0.0061 | Nerves           | 0.0068 |
| Prostate            | 0.0000 | Prostate         | 0.0155 |
| Sensory organs      | 0.0251 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

Electronic Northern for SEQ. ID NO.: 73

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0013      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0007      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0139 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

Electronic Northern for SEQ. ID NO.: 75

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0013      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0025      | 0.0000 | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0011      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0010      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0009      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0012 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0037 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 77

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0351      | 0.0051      | 6.8645 | 0.1457 |
| Breast               | 0.0026      | 0.0019      | 1.3611 | 0.7347 |
| Small intestine      | 0.0061      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0000      | 0.0104      | 0.0000 | undef  |
| Endocrine tissue     | 0.0034      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0019      | 0.0093      | 0.2071 | 4.8289 |
| Brain                | 0.0067      | 0.0010      | 6.4796 | 0.1543 |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0095      | 0.0000      | undef  | 0.0000 |
| Heart                | 0.0117      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0010      | 0.0041      | 0.2540 | 3.9367 |
| Stomach-esophagus    | 0.0097      | 0.0077      | 1.2605 | 0.7933 |
| Muscle-skeleton      | 0.0017      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0054      | 0.0137      | 0.3965 | 2.5213 |
| Pancreas             | 0.0017      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0060      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0229      | 0.0000      | undef  | 0.0000 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0032      |             |        |        |
| Prostate hyperplasia | 0.0030      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0035      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

| FETUS       | STANDARDIZED/SUBTRACTED |        |
|-------------|-------------------------|--------|
| % frequency | LIBRARIES               |        |
|             | % frequency             |        |
|             | Breast                  | 0.0000 |
| 0.0000      | Ovary_n                 | 0.0000 |
| 0.0056      | Ovary_t                 | 0.0100 |
| 0.0000      | Endocrine tissue        | 0.0000 |
| 0.0000      | Fetal                   | 0.0080 |
| 0.0000      | Gastrointestinal        | 0.0000 |
| 0.0000      | Hematopoietic           | 0.0050 |
| 0.0000      | Skin-muscle             | 0.0130 |
| 0.0072      | Testicles               | 0.0000 |
| 0.0000      | Lung                    | 0.0090 |
| 0.0000      | Nerves                  | 0.0060 |
| 0.0000      | Prostate                | 0.0000 |
| 0.0000      | Sensory Organs          | 0.0450 |
| 0.0000      | Uterus_n                |        |

## Electronic Northern for SEQ. ID NO.: 78

|                      | NORMAL      | TUMOR       | Ratios |         |
|----------------------|-------------|-------------|--------|---------|
|                      | % frequency | % frequency | N/T    | T/N     |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000  |
| Breast               | 0.0000      | 0.0000      | undef  | undef   |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef   |
| Ovary                | 0.0000      | 0.0000      | undef  | undef   |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef   |
| Gastrointestinal     | 0.0000      | 0.0093      | 0.0000 | undef   |
| Brain                | 0.0000      | 0.0000      | undef  | undef   |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef   |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef   |
| Heart                | 0.0011      | 0.0412      | 0.0257 | 38.9118 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef   |
| Lung                 | 0.0000      | 0.0020      | 0.0000 | undef   |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef   |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef   |
| Kidney               | 0.0000      | 0.0000      | undef  | undef   |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef   |
| Penis                | 0.0000      | 0.0000      | undef  | undef   |
| Prostate             | 0.0000      | 0.0000      | undef  | undef   |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef   |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef   |
| Uterus-general       | 0.0000      |             |        |         |
| Breast hyperplasia   | 0.0000      |             |        |         |
| Prostate hyperplasia | 0.0000      |             |        |         |
| Seminal vesicle      | 0.0000      |             |        |         |
| Sensory organs       | 0.0000      |             |        |         |
| White blood cells    | 0.0000      |             |        |         |
| Cervix               |             |             |        |         |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0278 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

Electronic Northern for SEQ. ID NO.: 79

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0351      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

| FETUS               |             | STANDARDIZED/SUBTRACTED |             |
|---------------------|-------------|-------------------------|-------------|
|                     | % frequency | LIBRARIES               | % frequency |
| Development         | 0.0000      | Breast                  | 0.0000      |
| Gastrointestinal    | 0.0000      | Ovary_n                 | 0.0000      |
| Brain               | 0.0000      | Ovary_t                 | 0.0000      |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000      |
| Skin                | 0.0000      | Fetal                   | 0.0000      |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000      |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000      |
| Lung                | 0.0000      | Skin-muscle             | 0.0000      |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000      |
| Kidney              | 0.0000      | Lung                    | 0.0000      |
| Placenta            | 0.0000      | Nerves                  | 0.0000      |
| Prostate            | 0.0000      | Prostate                | 0.0000      |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000      |
|                     |             | Uterus_n                |             |

## Electronic Northern for SEQ. ID NO.: 80

|                      | NORMAL      | TUMOR       | Ratio  | T/N    |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    |        |
| Bladder              | 0.0624      | 0.0102      | 6.1018 | 0.1639 |
| Breast               | 0.0141      | 0.0056      | 2.4953 | 0.4008 |
| Small intestine      | 0.0215      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0150      | 0.0078      | 1.9188 | 0.5212 |
| Endocrine tissue     | 0.0187      | 0.0050      | 3.7359 | 0.2677 |
| Gastrointestinal     | 0.0307      | 0.0139      | 2.2089 | 0.4527 |
| Brain                | 0.0214      | 0.0082      | 2.6099 | 0.3832 |
| Hematopoietic        | 0.0053      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0147      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0190      | 0.0065      | 2.9412 | 0.3400 |
| Heart                | 0.0360      | 0.0137      | 2.6213 | 0.3815 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0083      | 0.0041      | 2.0321 | 0.4921 |
| Stomach-esophagus    | 0.0097      | 0.0000      | undef  | 0.0000 |
| Muscle-skeleton      | 0.0171      | 0.0060      | 2.8555 | 0.3502 |
| Kidney               | 0.0136      | 0.0548      | 0.2478 | 4.0351 |
| Pancreas             | 0.0083      | 0.0387      | 0.2137 | 4.6800 |
| Penis                | 0.0150      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0087      | 0.0064      | 1.3648 | 0.7327 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0255      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0288      |             |        |        |
| Prostate hyperplasia | 0.0119      |             |        |        |
| Seminal vesicle      | 0.1246      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0017      |             |        |        |
| Cervix               | 0.0000      |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0136 |
| Gastrointestinal    | 0.0028 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0012 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0036 | Hematopoietic    | 0.0000 |
| Lung                | 0.0108 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0077 |
| Kidney              | 0.0000 | Lung             | 0.0082 |
| Placenta            | 0.0000 | Nerves           | 0.0010 |
| Prostate            | 0.0000 | Prostate         | 0.0205 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0083 |

Electronic Northern for SEQ. ID NO.: 82

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0390                | 0.0000               | undef         | 0.0000 |
| Breast               | 0.0000                | 0.0000               | undef         | undef  |
| Small intestine      | 0.0000                | 0.0000               | undef         | undef  |
| Ovary                | 0.0000                | 0.0000               | undef         | undef  |
| Endocrine tissue     | 0.0017                | 0.0000               | undef         | 0.0000 |
| Gastrointestinal     | 0.0000                | 0.0000               | undef         | undef  |
| Brain                | 0.0000                | 0.0000               | undef         | undef  |
| Hematopoietic        | 0.0000                | 0.0000               | undef         | 0.0000 |
| Skin                 | 0.0037                | 0.0000               | undef         | undef  |
| Hepatic              | 0.0000                | 0.0000               | undef         | 0.0000 |
| Heart                | 0.0011                | 0.0000               | undef         | undef  |
| Testicles            | 0.0000                | 0.0000               | undef         | undef  |
| Lung                 | 0.0000                | 0.0000               | undef         | undef  |
| Stomach-esophagus    | 0.0000                | 0.0000               | undef         | undef  |
| Muscle-skeleton      | 0.0000                | 0.0000               | undef         | undef  |
| Kidney               | 0.0000                | 0.0000               | undef         | undef  |
| Pancreas             | 0.0000                | 0.0000               | undef         | undef  |
| Penis                | 0.0000                | 0.0000               | undef         | undef  |
| Prostate             | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-endometrium   | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-myometrium    | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-general       | 0.0000                |                      |               |        |
| Breast hyperplasia   | 0.0000                |                      |               |        |
| Prostate hyperplasia | 0.0000                |                      |               |        |
| Seminal vesicle      | 0.0000                |                      |               |        |
| Sensory organs       | 0.0000                |                      |               |        |
| White blood cells    | 0.0000                |                      |               |        |
| Cervix               |                       |                      |               |        |

|                     | FETUS<br>% frequency | STANDARDIZED/SUBTRACTED<br>LIBRARIES<br>% frequency |        |
|---------------------|----------------------|---|--------|
| Development         | 0.0000               | Breast  | 0.0000 |
| Gastrointestinal    | 0.0000               | Ovary_n   | 0.0000 |
| Brain               | 0.0000               | Ovary_t   | 0.0000 |
| Hematopoietic       | 0.0000               | Endocrine tissue                                    | 0.0000 |
| Skin                | 0.0000               | Fetal   | 0.0000 |
| Hepatic             | 0.0000               | Gastrointestinal                                    | 0.0000 |
| Heart-blood vessels | 0.0000               | Hematopoietic                                       | 0.0000 |
| Lung                | 0.0000               | Skin-muscle   | 0.0000 |
| Suprarenal gland    | 0.0000               | Testicles   | 0.0000 |
| Kidney              | 0.0000               | Lung  | 0.0000 |
| Placenta            | 0.0000               | Nerves  | 0.0000 |
| Prostate            | 0.0000               | Prostate  | 0.0000 |
| Sensory organs      | 0.0000               | Sensory Organs                                      | 0.0000 |
|                     |                      | Uterus_n  |        |



Electronic Northern for SEQ. ID NO.: 83

|  | NORMAL      | TUMOR       | Ratios |     |
|--|-------------|-------------|--------|-----|
|  | % frequency | % frequency | N/T    | T/N |

|                      |        |        |         |        |
|----------------------|--------|--------|---------|--------|
| Bladder              | 0.0273 | 0.0026 | 10.6781 | 0.0936 |
| Breast               | 0.0013 | 0.0000 | undef   | 0.0000 |
| Small intestine      | 0.0061 | 0.0000 | undef   | 0.0000 |
| Ovary                | 0.0000 | 0.0000 | undef   | undef  |
| Endocrine tissue     | 0.0017 | 0.0025 | 0.6792  | 1.4722 |
| Gastrointestinal     | 0.0000 | 0.0000 | undef   | undef  |
| Brain                | 0.0229 | 0.0031 | 7.4396  | 0.1344 |
| Hematopoietic        | 0.0013 | 0.0000 | undef   | 0.0000 |
| Skin                 | 0.0000 | 0.0000 | undef   | undef  |
| Hepatic              | 0.0000 | 0.0000 | undef   | undef  |
| Heart                | 0.0011 | 0.0000 | undef   | 0.0000 |
| Testicles            | 0.0000 | 0.0000 | undef   | undef  |
| Lung                 | 0.0052 | 0.0000 | undef   | 0.0000 |
| Stomach-esophagus    | 0.0000 | 0.0000 | undef   | undef  |
| Muscle-skeleton      | 0.0017 | 0.0000 | undef   | 0.0000 |
| Kidney               | 0.0000 | 0.0000 | undef   | undef  |
| Pancreas             | 0.0050 | 0.0000 | undef   | 0.0000 |
| Penis                | 0.0000 | 0.0000 | undef   | undef  |
| Prostate             | 0.0044 | 0.0021 | 2.0473  | 0.4885 |
| Uterus-endometrium   | 0.0000 | 0.0000 | undef   | undef  |
| Uterus-myometrium    | 0.0000 | 0.0000 | undef   | undef  |
| Uterus-general       | 0.0000 | 0.0000 | undef   | undef  |
| Breast hyperplasia   | 0.0000 |        |         |        |
| Prostate hyperplasia | 0.0000 |        |         |        |
| Seminal vesicle      | 0.0000 |        |         |        |
| Sensory organs       | 0.0000 |        |         |        |
| White blood cells    | 0.0000 |        |         |        |
| Cervix               |        |        |         |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0068 |
| Gastrointestinal    | 0.0028 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0253 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0006 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0201 |
| Placenta            | 0.0061 | Nerves           | 0.0068 |
| Prostate            | 0.0000 | Prostate         | 0.0310 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

1090000 0400000000

Electronic Northern for SEQ. ID NO.: 85

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               | 0.0000      |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         |        |

Electronic Northern for SEQ. ID NO.: 86

|  | NORMAL      | TUMOR       | Ratios |     |
|--|-------------|-------------|--------|-----|
|  | % frequency | % frequency | N/T    | T/N |

|                      |        |        |        |        |
|----------------------|--------|--------|--------|--------|
| Bladder              | 0.0273 | 0.0051 | 5.3391 | 0.1873 |
| Breast               | 0.0000 | 0.0000 | undef  | undef  |
| Small intestine      | 0.0031 | 0.0000 | undef  | 0.0000 |
| Ovary                | 0.0000 | 0.0000 | undef  | undef  |
| Endocrine tissue     | 0.0017 | 0.0000 | undef  | 0.0000 |
| Gastrointestinal     | 0.0013 | 0.0000 | undef  | 0.0000 |
| Brain                | 0.0000 | 0.0010 | 0.0000 | undef  |
| Hematopoietic        | 0.0000 | 0.0000 | undef  | undef  |
| Skin                 | 0.0037 | 0.0000 | undef  | 0.0000 |
| Hepatic              | 0.0000 | 0.0000 | undef  | undef  |
| Heart                | 0.0011 | 0.0000 | undef  | 0.0000 |
| Testicles            | 0.0000 | 0.0000 | undef  | undef  |
| Lung                 | 0.0021 | 0.0041 | 0.5080 | 1.9684 |
| Stomach-esophagus    | 0.0000 | 0.0000 | undef  | undef  |
| Muscle-skeleton      | 0.0000 | 0.0060 | 0.0000 | undef  |
| Kidney               | 0.0000 | 0.0000 | undef  | undef  |
| Pancreas             | 0.0000 | 0.0000 | undef  | undef  |
| Penis                | 0.0030 | 0.0000 | undef  | 0.0000 |
| Prostate             | 0.0044 | 0.0000 | undef  | 0.0000 |
| Uterus-endometrium   | 0.0000 | 0.0000 | undef  | undef  |
| Uterus-myometrium    | 0.0000 | 0.0000 | undef  | undef  |
| Uterus-general       | 0.0000 | 0.0000 | undef  | undef  |
| Breast hyperplasia   | 0.0000 |        |        |        |
| Prostate hyperplasia | 0.0000 |        |        |        |
| Seminal vesicle      | 0.0000 |        |        |        |
| Sensory organs       | 0.0009 |        |        |        |
| White blood cells    | 0.0000 |        |        |        |
| Cervix               |        |        |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0139 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0012 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0036 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 88

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0051      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0007      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0011      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0021      | 0.0020      | 1.0161 | 0.9842 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0022      | 0.0043      | 0.5118 | 1.9538 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0009      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0068 |
| Gastrointestinal    | 0.0028      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0051 |
| Hematopoietic       | 0.0039      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0052 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0122 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000 |
| Lung                | 0.0000      | Skin-muscle             | 0.0386 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0062      | Lung                    | 0.0000 |
| Placenta            | 0.0000      | Nerves                  | 0.0068 |
| Prostate            | 0.0000      | Prostate                | 0.0000 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0208 |
|                     |             | Uterus_n                |        |

Electronic Northern for SEQ. ID NO.: 90

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0312      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0015      | 0.0010      | 1.4399 | 0.6945 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0065      | 0.0000 | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |             |
|---------------------|-------------|-------------------------|-------------|
|                     | % frequency | LIBRARIES               | % frequency |
| Development         | 0.0000      | Breast                  | 0.0000      |
| Gastrointestinal    | 0.0000      | Ovary_n                 | 0.0000      |
| Brain               | 0.0000      | Ovary_t                 | 0.0000      |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000      |
| Skin                | 0.0000      | Fetal                   | 0.0006      |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000      |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000      |
| Lung                | 0.0000      | Skin-muscle             | 0.0000      |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000      |
| Kidney              | 0.0000      | Lung                    | 0.0000      |
| Placenta            | 0.0000      | Nerves                  | 0.0010      |
| Prostate            | 0.0000      | Prostate                | 0.0000      |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000      |
|                     |             | Uterus_n                | 0.0000      |

## Electronic Northern for SEQ. ID NO.: 92

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0312      | 0.0051      | 6.1018 | 0.1639 |
| Breast               | 0.0102      | 0.0113      | 0.9074 | 1.1021 |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0051      | 0.0125      | 0.4075 | 2.4537 |
| Gastrointestinal     | 0.0077      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0067      | 0.0329      | 0.2025 | 4.9386 |
| Hematopoietic        | 0.0080      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0330      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0333      | 0.0323      | 1.0294 | 0.9714 |
| Heart                | 0.0127      | 0.0137      | 0.9252 | 1.0809 |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0156      | 0.0082      | 1.9051 | 0.5249 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0051      | 0.0120      | 0.4283 | 2.3347 |
| Kidney               | 0.0027      | 0.0205      | 0.1322 | 7.5658 |
| Pancreas             | 0.0050      | 0.0110      | 0.4487 | 2.2286 |
| Penis                | 0.0060      | 0.0267      | 0.2246 | 4.4517 |
| Prostate             | 0.0131      | 0.0128      | 1.0236 | 0.9769 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0102      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0128      |             |        |        |
| Prostate hyperplasia | 0.0208      |             |        |        |
| Seminal vesicle      | 0.0089      |             |        |        |
| Sensory organs       | 0.0118      |             |        |        |
| White blood cells    | 0.0147      |             |        |        |
| Cervix               | 0.0000      |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0340 |
| Gastrointestinal    | 0.0056      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0608 |
| Hematopoietic       | 0.0079      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0198 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0036      | Hematopoietic           | 0.0171 |
| Lung                | 0.0072      | Skin-muscle             | 0.0032 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0020 |
| Placenta            | 0.0545      | Nerves                  | 0.0068 |
| Prostate            | 0.0000      | Prostate                | 0.0697 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                |        |

## Electronic Northern for SEQ. ID NO.: 93

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0234      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0166      | 0.0226      | 0.7372 | 1.3564 |
| Small intestine      | 0.0000      | 0.0165      | 0.0000 | undef  |
| Ovary                | 0.0270      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0238      | 0.0276      | 0.8645 | 1.1567 |
| Gastrointestinal     | 0.0115      | 0.0093      | 1.2425 | 0.8048 |
| Brain                | 0.0089      | 0.0072      | 1.2342 | 0.8102 |
| Hematopoietic        | 0.0027      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0220      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0143      | 0.0518      | 0.2757 | 3.6266 |
| Heart                | 0.0148      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0230      | 0.0117      | 1.9679 | 0.5082 |
| Lung                 | 0.0218      | 0.0266      | 0.8207 | 1.2185 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0120      | 0.0120      | 0.9994 | 1.0006 |
| Kidney               | 0.0081      | 0.0137      | 0.5948 | 1.6813 |
| Pancreas             | 0.0149      | 0.0221      | 0.6731 | 1.4857 |
| Penis                | 0.0180      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0240      | 0.0213      | 1.1260 | 0.8881 |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0229      | 0.0340      | 0.6734 | 1.4851 |
| Uterus-general       | 0.0204      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0224      |             |        |        |
| Prostate hyperplasia | 0.0208      |             |        |        |
| Seminal vesicle      | 0.0445      |             |        |        |
| Sensory organs       | 0.0235      |             |        |        |
| White blood cells    | 0.0009      |             |        |        |
| Cervix               | 0.0213      |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0167 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0079 | Endocrine tissue | 0.0245 |
| Skin                | 0.0000 | Fetal            | 0.0099 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0065 |
| Lung                | 0.0108 | Skin-muscle      | 0.0154 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0020 |
| Placenta            | 0.0061 | Nerves           | 0.0068 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0042 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 94

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0195      | 0.0026      | 7.6272 | 0.1311 |
| Breast               | 0.0051      | 0.0094      | 0.5444 | 1.8368 |
| Small intestine      | 0.0092      | 0.0165      | 0.5561 | 1.7982 |
| Ovary                | 0.0000      | 0.0052      | 0.0000 | undef  |
| Endocrine tissue     | 0.0119      | 0.0150      | 0.7925 | 1.2619 |
| Gastrointestinal     | 0.0019      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0030      | 0.0103      | 0.2890 | 3.4724 |
| Hematopoietic        | 0.0067      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0032      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0052      | 0.0020      | 2.5402 | 0.3937 |
| Stomach-esophagus    | 0.0000      | 0.0153      | 0.0000 | undef  |
| Muscle-skeleton      | 0.0017      | 0.0120      | 0.1428 | 7.0040 |
| Kidney               | 0.0081      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0050      | 0.0055      | 0.8974 | 1.1143 |
| Penis                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0022      | 0.0043      | 0.5118 | 1.9538 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0381      | 0.0068      | 5.6113 | 0.1782 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0096      |             |        |        |
| Prostate hyperplasia | 0.0089      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0095      |             |        |        |
| White blood cells    | 0.0106      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |             |
|---------------------|-------------|-------------------------|-------------|
|                     | % frequency | LIBRARIES               | % frequency |
| Development         | 0.0000      | Breast                  | 0.0204      |
| Gastrointestinal    | 0.0028      | Ovary_n                 | 0.0000      |
| Brain               | 0.0000      | Ovary_t                 | 0.0709      |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000      |
| Skin                | 0.2513      | Fetal                   | 0.0070      |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000      |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0228      |
| Lung                | 0.0036      | Skin-muscle             | 0.0194      |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000      |
| Kidney              | 0.0185      | Lung                    | 0.0010      |
| Placenta            | 0.0061      | Nerves                  | 0.0000      |
| Prostate            | 0.0000      | Prostate                | 0.0000      |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0250      |
|                     |             | Uterus_n                |             |



## Electronic Northern for SEQ. ID NO.: 95

|                      | NORMAL      | TUMOR       | Ratios  |        |
|----------------------|-------------|-------------|---------|--------|
|                      | % frequency | % frequency | N/T     | T/N    |
| Bladder              | 0.0351      | 0.0026      | 13.7290 | 0.0729 |
| Breast               | 0.0026      | 0.0094      | 0.2722  | 3.6736 |
| Small intestine      | 0.0031      | 0.0000      | undef   | 0.0000 |
| Ovary                | 0.0000      | 0.0026      | 0.0000  | undef  |
| Endocrine tissue     | 0.0000      | 0.0075      | 0.0000  | undef  |
| Gastrointestinal     | 0.0000      | 0.0093      | 0.0000  | undef  |
| Brain                | 0.0037      | 0.0051      | 0.7200  | 1.3890 |
| Hematopoietic        | 0.0027      | 0.0000      | undef   | 0.0000 |
| Skin                 | 0.0073      | 0.0000      | undef   | 0.0000 |
| Hepatic              | 0.0190      | 0.0129      | 1.4706  | 0.6800 |
| Heart                | 0.0064      | 0.0000      | undef   | 0.0000 |
| Testicles            | 0.0058      | 0.0117      | 0.4920  | 2.0326 |
| Lung                 | 0.0021      | 0.0061      | 0.3387  | 2.9526 |
| Stomach-esophagus    | 0.0000      | 0.0077      | 0.0000  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0060      | 0.0000  | undef  |
| Kidney               | 0.0081      | 0.0068      | 1.1896  | 0.8406 |
| Pancreas             | 0.0050      | 0.0166      | 0.2991  | 3.3428 |
| Penis                | 0.0060      | 0.0000      | undef   | 0.0000 |
| Prostate             | 0.0044      | 0.0106      | 0.4095  | 2.4423 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef   | undef  |
| Uterus-myometrium    | 0.0000      | 0.0068      | 0.0000  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef   | undef  |
| Breast hyperplasia   | 0.0000      |             |         |        |
| Prostate hyperplasia | 0.0000      |             |         |        |
| Seminal vesicle      | 0.0000      |             |         |        |
| Sensory organs       | 0.0061      |             |         |        |
| White blood cells    | 0.0000      |             |         |        |
| Cervix               |             |             |         |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0028 | Ovary_n          | 0.0000 |
| Brain               | 0.0063 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0079 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0116 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0016 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0194 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0062 | Lung             | 0.0082 |
| Placenta            | 0.0000 | Nerves           | 0.0010 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0251 | Sensory Organs   | 0.0155 |
|                     |        | Uterus_n         | 0.0208 |

## Electronic Northern for SEQ. ID NO.: 96

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0195                | 0.0000               | undef         | 0.0000 |
| Breast               | 0.0090                | 0.0094               | 0.9527        | 1.0496 |
| Small intestine      | 0.0000                | 0.0000               | undef         | undef  |
| Ovary                | 0.0000                | 0.0000               | undef         | undef  |
| Endocrine tissue     | 0.0153                | 0.0176               | 0.8733        | 1.1451 |
| Gastrointestinal     | 0.0096                | 0.0185               | 0.5177        | 1.9316 |
| Brain                | 0.0081                | 0.0031               | 2.6399        | 0.3789 |
| Hematopoietic        | 0.0013                | 0.0000               | undef         | 0.0000 |
| Skin                 | 0.0000                | 0.0000               | undef         | undef  |
| Hepatic              | 0.0095                | 0.0000               | undef         | 0.0000 |
| Heart                | 0.0011                | 0.0000               | undef         | 0.0000 |
| Testicles            | 0.0000                | 0.0000               | undef         | undef  |
| Lung                 | 0.0052                | 0.0020               | 2.5402        | 0.3937 |
| Stomach-esophagus    | 0.0000                | 0.0000               | undef         | undef  |
| Muscle-skeleton      | 0.0017                | 0.0000               | undef         | 0.0000 |
| Kidney               | 0.0054                | 0.0000               | undef         | 0.0000 |
| Pancreas             | 0.0050                | 0.0055               | 0.8974        | 1.1143 |
| Penis                | 0.0180                | 0.0000               | undef         | 0.0000 |
| Prostate             | 0.0022                | 0.0064               | 0.3412        | 2.9308 |
| Uterus-endometrium   | 0.0135                | 0.0528               | 0.2561        | 3.9053 |
| Uterus-myometrium    | 0.0076                | 0.0136               | 0.5611        | 1.7821 |
| Uterus-general       | 0.0000                | 0.0000               | undef         | undef  |
| Breast hyperplasia   | 0.0000                |                      |               |        |
| Prostate hyperplasia | 0.0089                |                      |               |        |
| Seminal vesicle      | 0.0000                |                      |               |        |
| Sensory organs       | 0.0000                |                      |               |        |
| White blood cells    | 0.0000                |                      |               |        |
| Cervix               |                       |                      |               |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0139 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0083 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0051 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0099 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0071 | Hematopoietic    | 0.0000 |
| Lung                | 0.0072 | Skin-muscle      | 0.0324 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0062 | Lung             | 0.0328 |
| Placenta            | 0.0061 | Nerves           | 0.0141 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0251 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0167 |

## Electronic Northern for SEQ. ID NO.: 97

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0195                | 0.0000               | undef         | 0.0000 |
| Breast               | 0.0064                | 0.0038               | 1.7013        | 0.5878 |
| Small intestine      | 0.0061                | 0.0000               | undef         | 0.0000 |
| Ovary                | 0.0030                | 0.0156               | 0.1919        | 5.2117 |
| Endocrine tissue     | 0.0136                | 0.0251               | 0.5434        | 1.8403 |
| Gastrointestinal     | 0.0134                | 0.0139               | 0.9664        | 1.0348 |
| Brain                | 0.0074                | 0.0277               | 0.2667        | 3.7502 |
| Hematopoietic        | 0.0134                | 0.0000               | undef         | 0.0000 |
| Skin                 | 0.0037                | 0.0000               | undef         | 0.0000 |
| Hepatic              | 0.0048                | 0.0065               | 0.7353        | 1.3600 |
| Heart                | 0.0127                | 0.0412               | 0.3084        | 3.2426 |
| Testicles            | 0.0115                | 0.0585               | 0.1968        | 5.0816 |
| Lung                 | 0.0104                | 0.0204               | 0.5080        | 1.9684 |
| Stomach-esophagus    | 0.0193                | 0.0230               | 0.8404        | 1.1900 |
| Muscle-skeleton      | 0.0120                | 0.0240               | 0.4997        | 2.0011 |
| Kidney               | 0.0054                | 0.0068               | 0.7930        | 1.2610 |
| Pancreas             | 0.0083                | 0.0331               | 0.2493        | 4.0114 |
| Penis                | 0.0030                | 0.0000               | undef         | 0.0000 |
| Prostate             | 0.0240                | 0.0277               | 0.8661        | 1.1545 |
| Uterus-endometrium   | 0.0000                | 0.1055               | 0.0000        | undef  |
| Uterus-myometrium    | 0.0152                | 0.0000               | undef         | 0.0000 |
| Uterus-general       | 0.0153                | 0.0000               | undef         | 0.0000 |
| Breast hyperplasia   | 0.0064                | 0.0178               |               |        |
| Prostate hyperplasia | 0.0078                | 0.0089               |               |        |
| Seminal vesicle      | 0.0000                | 0.0000               |               |        |
| Sensory organs       | 0.0113                | 0.0000               |               |        |
| White blood cells    | 0.0000                |                      |               |        |
| Cervix               |                       |                      |               |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0111 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0039 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0036 |
| Lung                | 0.0181 |
| Suprarenal gland    | 0.0000 |
| Kidney              | 0.0124 |
| Placenta            | 0.0000 |
| Prostate            | 0.0249 |
| Sensory organs      | 0.0000 |

|                  |        |
|------------------|--------|
| Breast           | 0.0000 |
| Ovary_n          | 0.0000 |
| Ovary_t          | 0.0051 |
| Endocrine tissue | 0.0000 |
| Fetal            | 0.0012 |
| Gastrointestinal | 0.0122 |
| Hematopoietic    | 0.0000 |
| Skin-muscle      | 0.0065 |
| Testicles        | 0.0000 |
| Lung             | 0.0082 |
| Nerves           | 0.0070 |
| Prostate         | 0.0068 |
| Sensory Organs   | 0.0000 |
| Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 98

|                      | NORMAL      | TUMOR       | Ratios         | T/N |
|----------------------|-------------|-------------|----------------|-----|
|                      | % frequency | % frequency | N/T            |     |
| Bladder              | 0.0156      | 0.0000      | undef 0.0000   |     |
| Breast               | 0.0026      | 0.0113      | 0.2258 4.4083  |     |
| Small intestine      | 0.0031      | 0.0000      | undef 0.0000   |     |
| Ovary                | 0.0060      | 0.0026      | 2.3025 0.4343  |     |
| Endocrine tissue     | 0.0119      | 0.0100      | 1.1887 0.8413  |     |
| Gastrointestinal     | 0.0077      | 0.0000      | undef 0.0000   |     |
| Brain                | 0.0229      | 0.0062      | 3.7199 0.2688  |     |
| Hematopoietic        | 0.0027      | 0.0000      | undef 0.0000   |     |
| Skin                 | 0.0000      | 0.0847      | 0.0000 undef   |     |
| Hepatic              | 0.0095      | 0.0000      | undef 0.0000   |     |
| Heart                | 0.0032      | 0.0000      | undef 0.0000   |     |
| Testicles            | 0.0115      | 0.0000      | undef 0.0000   |     |
| Lung                 | 0.0062      | 0.0041      | 1.5241 0.6561  |     |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef undef    |     |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef undef    |     |
| Kidney               | 0.0027      | 0.0137      | 0.1983 5.0439  |     |
| Pancreas             | 0.0033      | 0.0055      | 0.5983 1.6714  |     |
| Penis                | 0.0090      | 0.0000      | undef 0.0000   |     |
| Prostate             | 0.0044      | 0.0064      | 0.6824 1.4654  |     |
| Uterus-endometrium   | 0.0000      | 0.0528      | 0.0000 undef   |     |
| Uterus-myometrium    | 0.0000      | 0.0136      | 0.0000 undef   |     |
| Uterus-general       | 0.0051      | 0.0954      | 0.0534 18.7357 |     |
| Breast hyperplasia   | 0.0000      |             |                |     |
| Prostate hyperplasia | 0.0000      |             |                |     |
| Seminal vesicle      | 0.0000      |             |                |     |
| Sensory organs       | 0.0061      |             |                |     |
| White blood cells    | 0.0106      |             |                |     |
| Cervix               |             |             |                |     |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0557 | Breast           | 0.0068 |
| Gastrointestinal    | 0.0083 | Ovary_n          | 0.0000 |
| Brain               | 0.0188 | Ovary_t          | 0.0051 |
| Hematopoietic       | 0.0039 | Endocrine tissue | 0.0245 |
| Skin                | 0.0000 | Fetal            | 0.0175 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0142 | Hematopoietic    | 0.0114 |
| Lung                | 0.0000 | Skin-muscle      | 0.0389 |
| Suprarenal gland    | 0.0254 | Testicles        | 0.0000 |
| Kidney              | 0.0062 | Lung             | 0.0164 |
| Placenta            | 0.0000 | Nerves           | 0.0251 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0251 | Sensory Organs   | 0.0310 |
|                     |        | Uterus_n         | 0.0209 |

## Electronic Northern for SEQ. ID NO.: 99

|                      | NORMAL<br>% frequency | TUMOR<br>% frequency | Ratios<br>N/T | T/N    |
|----------------------|-----------------------|----------------------|---------------|--------|
| Bladder              | 0.0312                | 0.0026               | 12.2035       | 0.0819 |
| Breast               | 0.0166                | 0.0132               | 1.2638        | 0.7912 |
| Small intestine      | 0.0061                | 0.0000               | undef         | 0.0000 |
| Ovary                | 0.0090                | 0.0026               | 3.4538        | 0.2895 |
| Endocrine tissue     | 0.0085                | 0.0025               | 3.3962        | 0.2944 |
| Gastrointestinal     | 0.0115                | 0.0231               | 0.4970        | 2.0121 |
| Brain                | 0.0074                | 0.0082               | 0.8999        | 1.1112 |
| Hematopoietic        | 0.0120                | 0.0379               | 0.3176        | 3.1487 |
| Skin                 | 0.0147                | 0.0000               | undef         | 0.0000 |
| Hepatic              | 0.0000                | 0.0000               | undef         | undef  |
| Heart                | 0.0085                | 0.0275               | 0.3084        | 3.2426 |
| Testicles            | 0.0058                | 0.0000               | undef         | 0.0000 |
| Lung                 | 0.0104                | 0.0061               | 1.6934        | 0.5905 |
| Stomach-esophagus    | 0.0193                | 0.0000               | undef         | 0.0000 |
| Muscle-skeleton      | 0.0051                | 0.0180               | 0.2856        | 3.5020 |
| Kidney               | 0.0109                | 0.0274               | 0.3965        | 2.5219 |
| Pancreas             | 0.0017                | 0.0000               | undef         | 0.0000 |
| Penis                | 0.0150                | 0.0000               | undef         | 0.0000 |
| Prostate             | 0.0022                | 0.0000               | undef         | 0.0000 |
| Uterus-endometrium   | 0.0203                | 0.0000               | undef         | 0.0000 |
| Uterus-myometrium    | 0.0000                | 0.0000               | undef         | undef  |
| Uterus-general       | 0.0255                | 0.0000               | undef         | 0.0000 |
| Breast hyperplasia   | 0.0224                |                      |               |        |
| Prostate hyperplasia | 0.0059                |                      |               |        |
| Seminal vesicle      | 0.0089                |                      |               |        |
| Sensory organs       | 0.0118                |                      |               |        |
| White blood cells    | 0.0113                |                      |               |        |
| Cervix               | 0.0106                |                      |               |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0139 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0111 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0051 |
| Hematopoietic       | 0.0039 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0035 |
| Hepatic             | 0.0260 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0107 | Hematopoietic    | 0.0057 |
| Lung                | 0.0036 | Skin-muscle      | 0.0130 |
| Suprarenal gland    | 0.0507 | Testicles        | 0.0000 |
| Kidney              | 0.0247 | Lung             | 0.0000 |
| Placenta            | 0.0061 | Nerves           | 0.0040 |
| Prostate            | 0.0000 | Prostate         | 0.0205 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0042 |

## Electronic Northern for SEQ. ID NO.: 100

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              |             |             |        |        |
| Breast               | 0.0156      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0031      | 0.0056      | 0.9074 | 1.1021 |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0030      | 0.0026      | 1.1513 | 0.8686 |
| Gastrointestinal     | 0.0000      | 0.0075      | 0.0000 | undef  |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0030      | 0.0051      | 0.5760 | 1.7362 |
| Skin                 | 0.0013      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0021      | 0.0137      | 0.1542 | 6.4853 |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0052      | 0.0041      | 1.2701 | 0.7873 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0034      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0000      | 0.0055      | 0.0000 | undef  |
| Penis                | 0.0060      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0044      | 0.0000      | undef  | 0.0000 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0136      | 0.0000 | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0032      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0089      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0061      |             |        |        |
| Cervix               | 0.0000      |             |        |        |

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0068 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0006 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0122 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0065 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0030 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0125 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 101

|                      | NORMAL      | TUMOR       | Ratios | T/N    |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    |        |
| Bladder              | 0.0234      | 0.0026      | 9.1527 | 0.1093 |
| Breast               | 0.0077      | 0.0094      | 0.8165 | 1.2245 |
| Small intestine      | 0.0123      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0060      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0034      | 0.0050      | 0.6792 | 1.4722 |
| Gastrointestinal     | 0.0057      | 0.0139      | 0.4142 | 2.4145 |
| Brain                | 0.0015      | 0.0021      | 0.7200 | 1.3890 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0048      | 0.0129      | 0.3676 | 2.7200 |
| Heart                | 0.0074      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0052      | 0.0020      | 2.5402 | 0.3937 |
| Stomach-esophagus    | 0.0097      | 0.0077      | 1.2605 | 0.7933 |
| Muscle-skeleton      | 0.0069      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0081      | 0.0137      | 0.5948 | 1.6813 |
| Pancreas             | 0.0000      | 0.0166      | 0.0000 | undef  |
| Penis                | 0.0150      | 0.0800      | 0.1872 | 5.3421 |
| Prostate             | 0.0109      | 0.0085      | 1.2795 | 0.7815 |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0076      | 0.0000      | undef  | 0.0000 |
| Uterus-general       | 0.0102      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0064      |             |        |        |
| Prostate hyperplasia | 0.0059      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0113      |             |        |        |
| White blood cells    | 0.0078      |             |        |        |
| Cervix               | 0.0213      |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |             |
|---------------------|-------------|-------------------------|-------------|
|                     | % frequency | LIBRARIES               | % frequency |
| Development         | 0.0000      | Breast                  | 0.0408      |
| Gastrointestinal    | 0.0056      | Ovary_n                 | 0.1595      |
| Brain               | 0.0000      | Ovary_t                 | 0.0101      |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000      |
| Skin                | 0.0000      | Petal                   | 0.0029      |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0122      |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000      |
| Lung                | 0.0108      | Skin-muscle             | 0.0130      |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0154      |
| Kidney              | 0.0000      | Lung                    | 0.0082      |
| Placenta            | 0.0000      | Nerves                  | 0.0000      |
| Prostate            | 0.0000      | Prostate                | 0.0000      |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000      |
|                     |             | Uterus_n                | 0.0000      |

## Electronic Northern for SEQ. ID NO.: 102

|                      | NORMAL      | TUMOR       | Ratios | T/N    |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    |        |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0026      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0025      | 0.0000 | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0015      | 0.0010      | 1.4399 | 0.6945 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0021      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0017      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0065      | 0.0021      | 3.0709 | 0.3256 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0102      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0030      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0204 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0039 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0070 |
| Hepatic             | 0.0260 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0000 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0137 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |



## Electronic Northern for SEQ. ID NO.: 103

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0019      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0000      | 0.0000      | undef  | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0000      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0000 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000 |
| Lung                | 0.0000      | Skin-muscle             | 0.0000 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0000 |
| Placenta            | 0.0000      | Nerves                  | 0.0000 |
| Prostate            | 0.0000      | Prostate                | 0.0000 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0000 |

Electronic Northern for SEQ. ID NO.: 104

|                      | NORMAL      | TUMOR       | Ratios | T/N     |
|----------------------|-------------|-------------|--------|---------|
|                      | % frequency | % frequency | N/T    |         |
| Bladder              | 0.0312      | 0.0051      | 6.1018 | 0.1639  |
| Breast               | 0.0102      | 0.0056      | 1.8147 | 0.5510  |
| Small intestine      | 0.0092      | 0.0000      | undef  | 0.0000  |
| Ovary                | 0.0180      | 0.0104      | 1.7269 | 0.5791  |
| Endocrine tissue     | 0.0085      | 0.0176      | 0.4852 | 2.0611  |
| Gastrointestinal     | 0.0172      | 0.0046      | 3.7275 | 0.2683  |
| Brain                | 0.0126      | 0.0123      | 1.0199 | 0.9804  |
| Hematopoietic        | 0.0040      | 0.0758      | 0.0529 | 18.8919 |
| Skin                 | 0.0257      | 0.0000      | undef  | 0.0000  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef   |
| Heart                | 0.0138      | 0.0275      | 0.5011 | 1.9955  |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000  |
| Lung                 | 0.0145      | 0.0102      | 1.4225 | 0.7030  |
| Stomach-esophagus    | 0.0000      | 0.0077      | 0.0000 | undef   |
| Muscle-skeleton      | 0.0206      | 0.0000      | undef  | 0.0000  |
| Kidney               | 0.0190      | 0.0137      | 1.3878 | 0.7206  |
| Pancreas             | 0.0050      | 0.0110      | 0.4487 | 2.2286  |
| Penis                | 0.0180      | 0.0000      | undef  | 0.0000  |
| Prostate             | 0.0087      | 0.0000      | undef  | 0.0000  |
| Uterus-endometrium   | 0.0203      | 0.0000      | undef  | 0.0000  |
| Uterus-myometrium    | 0.0152      | 0.0136      | 1.1223 | 0.8911  |
| Uterus-general       | 0.0153      | 0.0000      | undef  | 0.0000  |
| Breast hyperplasia   | 0.0096      |             |        |         |
| Prostate hyperplasia | 0.0149      |             |        |         |
| Seminal vesicle      | 0.0089      |             |        |         |
| Sensory organs       | 0.0353      |             |        |         |
| White blood cells    | 0.0043      |             |        |         |
| Cervix               | 0.0000      |             |        |         |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0204 |
| Gastrointestinal    | 0.0056      | Ovary_n                 | 0.1595 |
| Brain               | 0.0000      | Ovary_t                 | 0.0253 |
| Hematopoietic       | 0.0039      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0192 |
| Hepatic             | 0.0260      | Gastrointestinal        | 0.0122 |
| Heart-blood vessels | 0.0036      | Hematopoietic           | 0.0057 |
| Lung                | 0.0000      | Skin-muscle             | 0.0324 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0154 |
| Kidney              | 0.0185      | Lung                    | 0.0000 |
| Placenta            | 0.1030      | Nerves                  | 0.0151 |
| Prostate            | 0.0000      | Prostate                | 0.0000 |
| Sensory organs      | 0.0251      | Sensory Organs          | 0.0077 |
|                     |             | Uterus_n                | 0.0208 |

## Electronic Northern for SEQ. ID NO.: 105

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0115      | 0.0132      | 0.8750 | 1.1429 |
| Small intestine      | 0.0092      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0090      | 0.0052      | 1.7269 | 0.5791 |
| Endocrine tissue     | 0.0034      | 0.0050      | 0.6792 | 1.4722 |
| Gastrointestinal     | 0.0115      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0030      | 0.0041      | 0.7200 | 1.3890 |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0129      | 0.0000 | undef  |
| Heart                | 0.0127      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0117      | 0.0000 | undef  |
| Lung                 | 0.0042      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus    | 0.0097      | 0.0000      | undef  | 0.0000 |
| Muscle-skeleton      | 0.0051      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0027      | 0.0068      | 0.3965 | 2.5219 |
| Pancreas             | 0.0050      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0180      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0109      | 0.0085      | 1.2795 | 0.7815 |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0051      | 0.0000      | undef  | u.0000 |
| Breast hyperplasia   | 0.0064      |             |        |        |
| Prostate hyperplasia | 0.0059      |             |        |        |
| Seminal vesicle      | 0.0178      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               | 0.0319      |             |        |        |

| FETUS               |             | STANDARDIZED/SUBTRACTED<br>LIBRARIES |             |
|---------------------|-------------|--------------------------------------|-------------|
|                     | % frequency |                                      | % frequency |
| Development         | 0.0000      | Breast                               | 0.0000      |
| Gastrointestinal    | 0.0028      | Ovary_n                              | 0.0000      |
| Brain               | 0.0125      | Ovary_t                              | 0.0051      |
| Hematopoietic       | 0.0000      | Endocrine tissue                     | 0.0000      |
| Skin                | 0.0000      | Fetal                                | 0.0099      |
| Hepatic             | 0.0000      | Gastrointestinal                     | 0.0122      |
| Heart-blood vessels | 0.0107      | Hematopoietic                        | 0.0000      |
| Lung                | 0.0108      | Skin-muscle                          | 0.0259      |
| Suprarenal gland    | 0.0254      | Testicles                            | 0.0000      |
| Kidney              | 0.0000      |                                      | 0.0082      |
| Placenta            | 0.0121      | Lung                                 | 0.0100      |
| Prostate            | 0.0249      | Nerves                               | 0.0000      |
| Sensory organs      | 0.0000      | Prostate                             | 0.0000      |
|                     |             | Sensory Organs                       | 0.0000      |
|                     |             | Uterus_n                             | 0.0042      |

## Electronic Northern for SEQ. ID NO.: 106

|                      | NORMAL      | TUMOR       | Ratios  |        |
|----------------------|-------------|-------------|---------|--------|
|                      | % frequency | % frequency | N/T     | T/N    |
| Bladder              | 0.0312      | 0.0077      | 4.0678  | 0.2458 |
| Breast               | 0.0192      | 0.0019      | 10.2079 | 0.0980 |
| Small intestine      | 0.0061      | 0.0000      | undef   | 0.0000 |
| Ovary                | 0.0060      | 0.0390      | 0.1535  | 6.5146 |
| Endocrine tissue     | 0.0068      | 0.0075      | 0.9057  | 1.1042 |
| Gastrointestinal     | 0.0057      | 0.0046      | 1.2425  | 0.8048 |
| Brain                | 0.0118      | 0.0164      | 0.7200  | 1.3890 |
| Hematopoietic        | 0.0080      | 0.0379      | 0.2117  | 4.7230 |
| Skin                 | 0.0184      | 0.0000      | undef   | 0.0000 |
| Hepatic              | 0.0000      | 0.0129      | 0.0000  | undef  |
| Heart                | 0.0191      | 0.0275      | 0.6939  | 1.4412 |
| Testicles            | 0.0000      | 0.0000      | undef   | undef  |
| Lung                 | 0.0239      | 0.0102      | 2.3370  | 0.4279 |
| Stomach-esophagus    | 0.0000      | 0.0307      | 0.0000  | undef  |
| Muscle-skeleton      | 0.0051      | 0.0240      | 0.2142  | 4.6693 |
| Kidney               | 0.0081      | 0.0137      | 0.5948  | 1.6813 |
| Pancreas             | 0.0033      | 0.0110      | 0.2991  | 3.3428 |
| Penis                | 0.0120      | 0.0000      | undef   | 0.0000 |
| Prostate             | 0.0022      | 0.0021      | 1.0236  | 0.9769 |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef   | 0.0000 |
| Uterus-myometrium    | 0.0000      | 0.0204      | 0.0000  | undef  |
| Uterus-general       | 0.0153      | 0.0000      | undef   | 0.0000 |
| Breast hyperplasia   | 0.0320      |             |         |        |
| Prostate hyperplasia | 0.0059      |             |         |        |
| Seminal vesicle      | 0.0178      |             |         |        |
| Sensory organs       | 0.0118      |             |         |        |
| White blood cells    | 0.0087      |             |         |        |
| Cervix               | 0.0319      |             |         |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | % frequency             |        |
| Development         | 0.0278      | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0167      | Ovary_n                 | 0.0000 |
| Brain               | 0.0125      | Ovary_t                 | 0.0203 |
| Hematopoietic       | 0.0079      | Endocrine tissue        | 0.0245 |
| Skin                | 0.0000      | Fetal                   | 0.0198 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0213      | Hematopoietic           | 0.0171 |
| Lung                | 0.0191      | Skin-muscle             | 0.0000 |
| Suprarenal gland    | 0.0507      | Testicles               | 0.0000 |
| Kidney              | 0.0062      | Lung                    | 0.0082 |
| Placenta            | 0.0121      | Nerves                  | 0.0161 |
| Prostate            | 0.0000      | Prostate                | 0.0137 |
| Sensory organs      | 0.2762      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0208 |

## Electronic Northern for SEQ. ID NO.: 107

|                      | NORMAL      | TUMOR       | Ratios | T/N    |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    |        |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0013      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0000      | Ovary_n                 | 0.0000 |
| Brain               | 0.0063      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0000 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000 |
| Lung                | 0.0000      | Skin-muscle             | 0.0032 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0000 |
| Placenta            | 0.0000      | Nerves                  | 0.0000 |
| Prostate            | 0.0000      | Prostate                | 0.0000 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                |        |

## Electronic Northern for SEQ. ID NO.: 108

|                      | NORMAL      | TUMOR       | Ratios |         |
|----------------------|-------------|-------------|--------|---------|
|                      | % frequency | % frequency | N/T    | T/N     |
| Bladder              | 0.0195      | 0.0000      | undef  | 0.0000  |
| Breast               | 0.0038      | 0.0036      | 0.6905 | 1.4694  |
| Small intestine      | 0.0061      | 0.0165      | 0.3707 | 2.6973  |
| Ovary                | 0.0030      | 0.0052      | 0.5756 | 1.7372  |
| Endocrine tissue     | 0.0017      | 0.0100      | 0.1698 | 5.8889  |
| Gastrointestinal     | 0.0096      | 0.0000      | undef  | 0.0000  |
| Brain                | 0.0022      | 0.0103      | 0.2160 | 4.6299  |
| Hematopoietic        | 0.0027      | 0.0758      | 0.0353 | 28.3379 |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef   |
| Heart                | 0.0042      | 0.0000      | undef  | 0.0000  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef   |
| Lung                 | 0.0125      | 0.0061      | 2.0321 | 0.4921  |
| Stomach-esophagus    | 0.0097      | 0.0000      | undef  | 0.0000  |
| Muscle-skeleton      | 0.0017      | 0.0000      | undef  | 0.0000  |
| Kidney               | 0.0000      | 0.0137      | 0.0000 | undef   |
| Pancreas             | 0.0000      | 0.0221      | 0.0000 | undef   |
| Penis                | 0.0000      | 0.0000      | undef  | undef   |
| Prostate             | 0.0065      | 0.0021      | 3.0709 | 0.3256  |
| Uterus-endometrium   | 0.0000      | 0.0528      | 0.0000 | undef   |
| Uterus-myometrium    | 0.0076      | 0.0000      | undef  | 0.0000  |
| Uterus-general       | 0.0051      | 0.0000      | undef  | 0.0000  |
| Breast hyperplasia   | 0.0032      |             |        |         |
| Prostate hyperplasia | 0.0059      |             |        |         |
| Seminal vesicle      | 0.0000      |             |        |         |
| Sensory organs       | 0.0118      |             |        |         |
| White blood cells    | 0.0095      |             |        |         |
| Cervix               | 0.0000      |             |        |         |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     |             | LIBRARIES               |        |
|                     | % frequency | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0056      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0759 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0000 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0057 |
| Lung                | 0.0000      | Skin-muscle             | 0.0000 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0164 |
| Placenta            | 0.0000      | Nerves                  | 0.0000 |
| Prostate            | 0.0000      | Prostate                | 0.0274 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0083 |

## Electronic Northern for SEQ. ID NO.: 109

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0507      | 0.0179      | 2.8330 | 0.3530 |
| Breast               | 0.0153      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0276      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0270      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0119      | 0.0075      | 1.5849 | 0.6309 |
| Gastrointestinal     | 0.0096      | 0.0046      | 2.0708 | 0.4829 |
| Brain                | 0.0044      | 0.0010      | 4.3198 | 0.2315 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0065      | 0.0000 | undef  |
| Heart                | 0.0201      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0115      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus    | 0.0580      | 0.0230      | 2.5211 | 0.3967 |
| Muscle-skeleton      | 0.0771      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0000      | 0.0068      | 0.0000 | undef  |
| Pancreas             | 0.0033      | 0.0221      | 0.1496 | 6.6857 |
| Penis                | 0.0210      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0174      | 0.0106      | 1.6378 | 0.6106 |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0229      | 0.0068      | 3.3668 | 0.2970 |
| Uterus-general       | 0.0357      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0096      |             |        |        |
| Prostate hyperplasia | 0.0149      |             |        |        |
| Seminal vesicle      | 0.0514      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               | 0.0000      |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0816 |
| Gastrointestinal    | 0.0083      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0039      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0041 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0244 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000 |
| Lung                | 0.0000      | Skin-muscle             | 0.0097 |
| Suprarenal gland    | 0.0507      | Testicles               | 0.0000 |
| Kidney              | 0.0062      | Lung                    | 0.0000 |
| Placenta            | 0.0242      | Nerves                  | 0.0030 |
| Prostate            | 0.0748      | Prostate                | 0.0000 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0042 |

## Electronic Northern for SEQ. ID NO.: 110

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0230      | 0.0038      | 6.1248 | 0.1633 |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0120      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0136      | 0.0025      | 5.4340 | 0.1840 |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0022      | 0.0031      | 0.7200 | 1.3990 |
| Hematopoietic        | 0.0027      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0184      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0065      | 0.0000 | undef  |
| Heart                | 0.0212      | 0.0137      | 1.5420 | 0.6485 |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0156      | 0.0164      | 0.9526 | 1.0498 |
| Lung                 | 0.0000      | 0.0077      | 0.0000 | undef  |
| Stomach-esophagus    | 0.0069      | 0.0180      | 0.3807 | 2.6265 |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0017      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0060      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0000      | 0.0043      | 0.0000 | undef  |
| Prostate             | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-endometrium   | 0.0305      | 0.0068      | 4.4891 | 0.2228 |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0192      |             |        |        |
| Breast hyperplasia   | 0.0089      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0235      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0532      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0417 | Breast           | 0.0204 |
| Gastrointestinal    | 0.0056 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0039 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0064 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0213 | Hematopoietic    | 0.0000 |
| Lung                | 0.0072 | Skin-muscle      | 0.0162 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0124 | Lung             | 0.0000 |
| Placenta            | 0.0121 | Nerves           | 0.0080 |
| Prostate            | 0.0249 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0125 |



## Electronic Northern for SEQ. ID NO.: 111

|                      | NORMAL      | TUMOR       | Ratios  | T/N     |
|----------------------|-------------|-------------|---------|---------|
|                      | % frequency | % frequency | N/T     |         |
| Bladder              | 0.0312      | 0.0026      | 12.2035 | 0.0819  |
| Breast               | 0.0051      | 0.0019      | 2.7221  | 0.3674  |
| Small intestine      | 0.0000      | 0.0000      | undef   | undef   |
| Ovary                | 0.0000      | 0.0025      | 0.0000  | undef   |
| Endocrine tissue     | 0.0017      | 0.0025      | 0.6792  | 1.4722  |
| Gastrointestinal     | 0.0038      | 0.0000      | undef   | 0.0000  |
| Brain                | 0.0022      | 0.0041      | 0.5400  | 1.8520  |
| Hematopoietic        | 0.0013      | 0.0000      | undef   | 0.0000  |
| Skin                 | 0.0000      | 0.0000      | undef   | undef   |
| Hepatic              | 0.0000      | 0.0065      | 0.0000  | undef   |
| Heart                | 0.0011      | 0.0137      | 0.0771  | 12.9706 |
| Testicles            | 0.0000      | 0.0000      | undef   | undef   |
| Lung                 | 0.0021      | 0.0020      | 1.0161  | 0.9842  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef   | undef   |
| Muscle-skeleton      | 0.0034      | 0.0000      | undef   | 0.0000  |
| Kidney               | 0.0081      | 0.0000      | undef   | 0.0000  |
| Pancreas             | 0.0017      | 0.0055      | 0.2991  | 3.3428  |
| Penis                | 0.0030      | 0.0000      | undef   | 0.0000  |
| Prostate             | 0.0044      | 0.0021      | 2.0473  | 0.4885  |
| Uterus-endometrium   | 0.0135      | 0.0000      | undef   | 0.0000  |
| Uterus-myometrium    | 0.0076      | 0.0000      | undef   | 0.0000  |
| Uterus-general       | 0.0051      | 0.0000      | undef   | 0.0000  |
| Breast hyperplasia   | 0.0000      | 0.0032      |         |         |
| Prostate hyperplasia | 0.0000      |             |         |         |
| Seminal vesicle      | 0.0000      |             |         |         |
| Sensory organs       | 0.0009      |             |         |         |
| White blood cells    | 0.0000      |             |         |         |
| Cervix               |             |             |         |         |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0340 |
| Gastrointestinal    | 0.0000      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0039      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0012 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000 |
| Lung                | 0.0000      | Skin-muscle             | 0.0065 |
| Suprarenal gland    | 0.0254      | Testicles               | 0.0000 |
| Kidney              | 0.0124      | Lung                    | 0.0082 |
| Placenta            | 0.0121      | Nerves                  | 0.0020 |
| Prostate            | 0.0000      | Nerves                  | 0.0205 |
| Sensory organs      | 0.0000      | Prostate                | 0.0000 |
|                     |             | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 112

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0013      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0000      | 0.0021      | 0.0000 | undef  |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0021      | 0.0137      | 0.1542 | 6.4853 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0010      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0027      | 0.0068      | 0.3965 | 2.5219 |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0000      | 0.0021      | 0.0000 | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0032      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0118      |             |        |        |
| Sensory organs       | 0.0043      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

| FETUS               |             | STANDARDIZED/SUBTRACTED LIBRARIES |             |
|---------------------|-------------|-----------------------------------|-------------|
|                     | % frequency |                                   | % frequency |
| Development         | 0.0000      | Breast                            | 0.0000      |
| Gastrointestinal    | 0.0023      | Ovary_n                           | 0.0000      |
| Brain               | 0.0000      | Ovary_t                           | 0.0000      |
| Hematopoietic       | 0.0000      | Endocrine tissue                  | 0.0000      |
| Skin                | 0.0000      | Fetal                             | 0.0017      |
| Hepatic             | 0.0000      | Gastrointestinal                  | 0.0122      |
| Heart-blood vessels | 0.0000      | Hematopoietic                     | 0.0114      |
| Lung                | 0.0000      | Skin-muscle                       | 0.0065      |
| Suprarenal gland    | 0.0000      | Testicles                         | 0.0154      |
| Kidney              | 0.0000      | Lung                              | 3.0092      |
| Placenta            | 0.0000      | Nerves                            | 0.0000      |
| Prostate            | 0.0000      | Prostate                          | 0.0000      |
| Sensory organs      | 0.0000      | Sensory Organs                    | 0.0000      |
|                     |             | Uterus_n                          | 0.0000      |

## Electronic Northern for SEQ. ID NO.: 113

|                      | NORMAL      | TUMOR       | Ratios  |         |
|----------------------|-------------|-------------|---------|---------|
|                      | % frequency | % frequency | N/T     | T/N     |
| Bladder              | 0.0312      | 0.0026      | 12.2035 | 0.0819  |
| Breast               | 0.0102      | 0.0019      | 5.4442  | 0.1837  |
| Small intestine      | 0.0031      | 0.0000      | undef   | 0.0000  |
| Ovary                | 0.0060      | 0.0000      | undef   | 0.0000  |
| Endocrine tissue     | 0.0000      | 0.0050      | 0.0000  | undef   |
| Gastrointestinal     | 0.0019      | 0.0000      | undef   | 0.0000  |
| Brain                | 0.0037      | 0.0031      | 1.1999  | 0.8334  |
| Hematopoietic        | 0.0000      | 0.0000      | undef   | undef   |
| Skin                 | 0.0037      | 0.0000      | undef   | 0.0000  |
| Hepatic              | 0.0000      | 0.0000      | undef   | undef   |
| Heart                | 0.0021      | 0.0000      | undef   | 0.0000  |
| Testicles            | 0.0000      | 0.0000      | undef   | undef   |
| Lung                 | 0.0042      | 0.0020      | 2.0321  | 0.4921  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef   | undef   |
| Muscle-skeleton      | 0.0017      | 0.0180      | 0.0952  | 10.5060 |
| Kidney               | 0.0054      | 0.0068      | 0.7930  | 1.2610  |
| Pancreas             | 0.0017      | 0.0055      | 0.2991  | 3.3428  |
| Penis                | 0.0030      | 0.0000      | undef   | 0.0000  |
| Prostate             | 0.0000      | 0.0000      | undef   | undef   |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef   | undef   |
| Uterus-myometrium    | 0.0102      | 0.0000      | undef   | 0.0000  |
| Uterus-general       | 0.0032      |             |         |         |
| Breast hyperplasia   | 0.0000      |             |         |         |
| Prostate hyperplasia | 0.0000      |             |         |         |
| Seminal vesicle      | 0.0706      |             |         |         |
| Sensory organs       | 0.0000      |             |         |         |
| White blood cells    | 0.0000      |             |         |         |
| Cervix               |             |             |         |         |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |             |
|---------------------|-------------|-------------------------|-------------|
|                     | % frequency | LIBRARIES               | % frequency |
| Development         | 0.0000      | Breast                  | 0.0136      |
| Gastrointestinal    | 0.0167      | Ovary_n                 | 0.0000      |
| Brain               | 0.0000      | Ovary_t                 | 0.0203      |
| Hematopoietic       | 0.0039      | Endocrine tissue        | 0.0000      |
| Skin                | 0.0000      | Fetal                   | 0.0140      |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000      |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000      |
| Lung                | 0.0036      | Skin-muscle             | 0.0000      |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000      |
| Kidney              | 0.0062      | Lung                    | 0.0000      |
| Placenta            | 0.0667      | Nerves                  | 0.0000      |
| Prostate            | 0.0249      | Prostate                | 0.0000      |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000      |
|                     |             | Uterus_n                | 0.0000      |

## Electronic Northern for SEQ. ID NO.: 114

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0039      | 0.0000 | undef  |
| Small intestine      | 0.0092      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0007      | 0.0031      | 0.2400 | 4.1669 |
| Hematopoietic        | 0.0027      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0021      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0021      | 0.0020      | 1.0161 | 0.9842 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0068      | 0.0000 | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0022      | 0.0000      | undef  | 0.0000 |
| Uterus-endometrium   | 0.0069      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0089      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0017      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0000      | Breast                  | 0.0068 |
| Gastrointestinal    | 0.0000      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0051 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0005 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0000      | Hematopoietic           | 0.0000 |
| Lung                | 0.0000      | Skin-muscle             | 0.0000 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0000 |
| Placenta            | 0.0000      | Nerves                  | 0.0000 |
| Prostate            | 0.0000      | Prostate                | 0.0000 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 115

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0195      | 0.0026      | 7.6272 | 0.1311 |
| Breast               | 0.0038      | 0.0019      | 2.0416 | 0.4898 |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0120      | 0.0052      | 2.3025 | 0.4343 |
| Endocrine tissue     | 0.0068      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0038      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0007      | 0.0051      | 0.1440 | 6.9448 |
| Hematopoietic        | 0.0027      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0129      | 0.0000 | undef  |
| Heart                | 0.0042      | 0.0137      | 0.3084 | 3.2426 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0034      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0066      | 0.0276      | 0.2393 | 4.1785 |
| Penis                | 0.0000      | 0.0267      | 0.0000 | undef  |
| Prostate             | 0.0022      | 0.0000      | undef  | 0.0000 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0076      | 0.0000      | undef  | 0.0000 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0089      |             |        |        |
| Prostate hyperplasia | 0.0178      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0035      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0139 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0028 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0017 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0057 |
| Lung                | 0.0036 | Skin-muscle      | 0.0130 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0062 | Lung             | 0.0020 |
| Placenta            | 0.0121 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0083 |
|                     |        | Uterus_n         |        |

## Electronic Northern for SEQ. ID NO.: 116

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0624      | 0.0204      | 3.0509 | 0.3278 |
| Breast               | 0.0102      | 0.0000      | undef  | 0.0000 |
| Small intestine      | 0.0368      | 0.0165      | 2.2244 | 0.4496 |
| Ovary                | 0.0120      | 0.0026      | 4.6050 | 0.2172 |
| Endocrine tissue     | 0.0000      | 0.0050      | 0.0000 | undef  |
| Gastrointestinal     | 0.0556      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0030      | 0.0041      | 0.7200 | 1.3890 |
| Hematopoietic        | 0.0053      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0110      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0190      | 0.0065      | 2.9412 | 0.3400 |
| Heart                | 0.0042      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0031      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus    | 0.0290      | 0.0230      | 1.2605 | 0.7933 |
| Muscle-skeleton      | 0.0103      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0033      | 0.0110      | 0.2991 | 3.3428 |
| Penis                | 0.1258      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0479      | 0.0319      | 1.5013 | 0.6661 |
| Uterus-endometrium   | 0.0338      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.1067      | 0.0272      | 3.9279 | 0.2546 |
| Uterus-general       | 0.0509      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0128      |             |        |        |
| Prostate hyperplasia | 0.0476      |             |        |        |
| Seminal vesicle      | 0.0267      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               | 0.0213      |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0167 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0118 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0071 |
| Lung                | 0.0000 |
| Suprarenal gland    | 0.0000 |
| Kidney              | 0.0000 |
| Placenta            | 0.0000 |
| Prostate            | 0.0499 |
| Sensory organs      | 0.0000 |

|                  |        |
|------------------|--------|
| Breast           | 0.0204 |
| Ovary_n          | 0.1595 |
| Ovary_t          | 0.0000 |
| Endocrine tissue | 0.0000 |
| Fetal            | 0.0082 |
| Gastrointestinal | 0.0610 |
| Hematopoietic    | 0.0000 |
| Skin-muscle      | 0.0032 |
| Testicles        | 0.0000 |
| Lung             | 0.0000 |
| Nerves           | 0.0060 |
| Prostate         | 0.0342 |
| Sensory Organs   | 0.0000 |
| Uterus_n         | 0.0541 |

## Electronic Northern for SEQ. ID NO.: 117

|                      | NORMAL      | TUMOR       | Ratios | T/N    |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    |        |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0000      | 0.0019      | 0.0000 | undef  |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0000      | 0.0000      | undef  | undef  |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0007      | 0.0000      | undef  | 0.0000 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0000      | 0.0000      | undef  | undef  |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0000      | undef  | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      |             |        |        |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0235      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

|                     |        |                  |        |
|---------------------|--------|------------------|--------|
| Development         | 0.0000 | Breast           | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n          | 0.0000 |
| Brain               | 0.0000 | Ovary_t          | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue | 0.0000 |
| Skin                | 0.0000 | Fetal            | 0.0000 |
| Hepatic             | 0.0000 | Gastrointestinal | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic    | 0.0000 |
| Lung                | 0.0072 | Skin-muscle      | 0.0000 |
| Suprarenal gland    | 0.0000 | Testicles        | 0.0000 |
| Kidney              | 0.0000 | Lung             | 0.0000 |
| Placenta            | 0.0000 | Nerves           | 0.0000 |
| Prostate            | 0.0000 | Prostate         | 0.0000 |
| Sensory organs      | 0.0000 | Sensory Organs   | 0.0000 |
|                     |        | Uterus_n         | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 118

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0026      | 0.0038      | 0.6805 | 1.4694 |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0030      | 0.0026      | 1.1513 | 0.8686 |
| Endocrine tissue     | 0.0068      | 0.0150      | 0.4528 | 2.2083 |
| Gastrointestinal     | 0.0000      | 0.0000      | undef  | undef  |
| Brain                | 0.0007      | 0.0051      | 0.1440 | 6.9449 |
| Hematopoietic        | 0.0027      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0065      | 0.0000 | undef  |
| Heart                | 0.0064      | 0.0137      | 0.4626 | 2.1618 |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0010      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0017      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0000      | 0.0110      | 0.0000 | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0044      | 0.0064      | 0.6824 | 1.4654 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0152      | 0.0068      | 2.2445 | 0.4455 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0089      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0026      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

| FETUS               |        | STANDARDIZED/SUBTRACTED |        |
|---------------------|--------|-------------------------|--------|
| % frequency         |        | LIBRARIES               |        |
|                     |        | % frequency             |        |
| Development         | 0.0000 | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0000 | Ovary_n                 | 0.1595 |
| Brain               | 0.0000 | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000 | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000 | Fetal                   | 0.0006 |
| Hepatic             | 0.0000 | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0000 | Hematopoietic           | 0.0114 |
| Lung                | 0.0000 | Skin-muscle             | 0.0063 |
| Suprarenal gland    | 0.0000 | Testicles               | 0.0154 |
| Kidney              | 0.0000 | Lung                    | 0.0000 |
| Placenta            | 0.0061 | Nerves                  | 0.0020 |
| Prostate            | 0.0000 | Prostate                | 0.0068 |
| Sensory organs      | 0.0000 | Sensory Organs          | 0.0077 |
|                     |        | Uterus_n                | 0.0000 |



## Electronic Northern for SEQ. ID NO.: 119

|                      | NORMAL      | TUMOR       | Ratios | T/N    |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    |        |
| Bladder              | 0.0819      | 0.0383      | 2.1356 | 0.4682 |
| Breast               | 0.0473      | 0.0320      | 1.4811 | 0.6752 |
| Small intestine      | 0.0460      | 0.0331      | 1.3903 | 0.7193 |
| Ovary                | 0.0539      | 0.0442      | 1.2190 | 0.8204 |
| Endocrine tissue     | 0.0494      | 0.0652      | 0.7576 | 1.3199 |
| Gastrointestinal     | 0.0805      | 0.0139      | 5.7984 | 0.1725 |
| Brain                | 0.0451      | 0.0390      | 1.1557 | 0.8653 |
| Hematopoietic        | 0.0374      | 0.0379      | 0.9881 | 1.0121 |
| Skin                 | 0.0367      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0190      | 0.0323      | 0.5882 | 1.7000 |
| Heart                | 0.0382      | 0.0825      | 0.4626 | 2.1618 |
| Testicles            | 0.0173      | 0.0117      | 1.4759 | 0.6775 |
| Lung                 | 0.0384      | 0.0184      | 2.0886 | 0.4788 |
| Stomach-esophagus    | 0.0580      | 0.0537      | 1.0805 | 0.9255 |
| Muscle-skeleton      | 0.0514      | 0.0240      | 2.1416 | 0.4669 |
| Kidney               | 0.0489      | 0.0479      | 1.0196 | 0.9808 |
| Pancreas             | 0.0330      | 0.0663      | 0.4986 | 2.0057 |
| Penis                | 0.0359      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0610      | 0.0617      | 0.9883 | 1.0118 |
| Uterus-endometrium   | 0.2838      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0305      | 0.0000      | undef  | 0.0000 |
| Uterus-general       | 0.0509      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.2206      |             |        |        |
| Prostate hyperplasia | 0.0773      |             |        |        |
| Seminal vesicle      | 0.0089      |             |        |        |
| Sensory organs       | 0.0353      |             |        |        |
| White blood cells    | 0.0737      |             |        |        |
| Cervix               | 0.0319      |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0278      | Breast                  | 0.0340 |
| Gastrointestinal    | 0.0361      | Ovary_n                 | 0.1595 |
| Brain               | 0.0125      | Ovary_t                 | 0.0101 |
| Hematopoietic       | 0.0157      | Endocrine tissue        | 0.0490 |
| Skin                | 0.0000      | Fetal                   | 0.0233 |
| Hepatic             | 0.0260      | Gastrointestinal        | 0.0488 |
| Heart-blood vessels | 0.0818      | Hematopoietic           | 0.0285 |
| Lung                | 0.0325      | Skin-muscle             | 0.0227 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0154 |
| Kidney              | 0.0432      | Lung                    | 0.0164 |
| Placenta            | 0.0303      | Nerves                  | 0.0261 |
| Prostate            | 0.0000      | Prostate                | 0.1163 |
| Sensory organs      | 0.0126      | Sensory Organs          | 0.0929 |
|                     |             | Uterus_n                | 0.0416 |

## Electronic Northern for SEQ. ID NO.: 120

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0195      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0026      | 0.0038      | 0.6805 | 1.4694 |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0017      | 0.0025      | 0.6792 | 1.4722 |
| Gastrointestinal     | 0.0038      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0052      | 0.0041      | 1.2599 | 0.7937 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0011      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0000      | 0.0020      | 0.0000 | undef  |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0034      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0000      | 0.0000      | undef  | undef  |
| Penis                | 0.0000      | 0.0000      | undef  | undef  |
| Prostate             | 0.0022      | 0.0000      | undef  | 0.0000 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0000      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0026      |             |        |        |
| White blood cells    | 0.0106      |             |        |        |
| Cervix               |             |             |        |        |

| FETUS       | STANDARDIZED/SUBTRACTED |        |
|-------------|-------------------------|--------|
| % frequency | LIBRARIES               |        |
|             | % frequency             |        |
| 0.0000      | Breast                  | 0.0000 |
| 0.0000      | Ovary_n                 | 0.0000 |
| 0.0000      | Ovary_t                 | 0.0000 |
| 0.0000      | Endocrine tissue        | 0.0000 |
| 0.0000      | Fetal                   | 0.0006 |
| 0.0000      | Gastrointestinal        | 0.0000 |
| 0.0000      | Hematopoietic           | 0.0000 |
| 0.0000      | Skin-muscle             | 0.0000 |
| 0.0254      | Testicles               | 0.0000 |
| 0.0062      | Lung                    | 0.0000 |
| 0.0000      | Nerves                  | 0.0070 |
| 0.0000      | Prostate                | 0.0000 |
| 0.0000      | Sensory Organs          | 0.0000 |
|             | Uterus_n                | 0.0000 |

## Electronic Northern for SEQ. ID NO.: 121

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0273      | 0.0051      | 5.3391 | 0.1873 |
| Breast               | 0.0000      | 0.0000      | undef  | undef  |
| Small intestine      | 0.0031      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0030      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0000      | 0.0025      | 0.0000 | undef  |
| Gastrointestinal     | 0.0038      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0059      | 0.0041      | 1.4399 | 0.6945 |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0000      | 0.0000      | undef  | undef  |
| Hepatic              | 0.0048      | 0.0000      | undef  | 0.0000 |
| Heart                | 0.0032      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0117      | 0.0000 | undef  |
| Lung                 | 0.0052      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus    | 0.0000      | 0.0077      | 0.0000 | undef  |
| Muscle-skeleton      | 0.0000      | 0.0000      | undef  | undef  |
| Kidney               | 0.0000      | 0.0000      | undef  | undef  |
| Pancreas             | 0.0017      | 0.0000      | undef  | 0.0000 |
| Penis                | 0.0150      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0109      | 0.0085      | 1.2795 | 0.7815 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0076      | 0.0000      | undef  | 0.0000 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0000      |             |        |        |
| Prostate hyperplasia | 0.0089      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

| FETUS               |             | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
| % frequency         |             | LIBRARIES               |        |
|                     | % frequency |                         |        |
| Development         | 0.0000      | Breast                  | 0.0136 |
| Gastrointestinal    | 0.0028      | Ovary_n                 | 0.1595 |
| Brain               | 0.0000      | Ovary_t                 | 0.0051 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0245 |
| Skin                | 0.0000      | Fetal                   | 0.0035 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0000 |
| Heart-blood vessels | 0.0036      | Hematopoietic           | 0.0000 |
| Lung                | 0.0036      | Skin-muscle             | 0.0032 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0077 |
| Kidney              | 0.0000      | Lung                    | 0.0000 |
| Placenta            | 0.0000      | Nerves                  | 0.0030 |
| Prostate            | 0.0000      | Prostate                | 0.0068 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0167 |

## Electronic Northern for SEQ. ID NO.: 122

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0351      | 0.0077      | 4.5763 | 0.2185 |
| Breast               | 0.0077      | 0.0038      | 2.0416 | 0.4899 |
| Small intestine      | 0.0184      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0000      | 0.0000      | undef  | undef  |
| Endocrine tissue     | 0.0017      | 0.0000      | undef  | 0.0000 |
| Gastrointestinal     | 0.0115      | 0.0093      | 1.2425 | 0.8048 |
| Brain                | 0.0030      | 0.0021      | 1.4399 | 0.6945 |
| Hematopoietic        | 0.0013      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0095      | 0.0000      | undef  | 0.0000 |
| Heart                | 0.0233      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000 |
| Lung                 | 0.0021      | 0.0000      | undef  | 0.0000 |
| Stomach-esophagus    | 0.0000      | 0.0077      | 0.0000 | undef  |
| Muscle-skeleton      | 0.0103      | 0.0000      | undef  | 0.0000 |
| Kidney               | 0.0054      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0000      | 0.0035      | 0.0000 | undef  |
| Penis                | 0.0599      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0131      | 0.0149      | 0.8774 | 1.1397 |
| Uterus-endometrium   | 0.0068      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0152      | 0.0340      | 0.4489 | 2.2276 |
| Uterus-general       | 0.0407      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0064      |             |        |        |
| Prostate hyperplasia | 0.0059      |             |        |        |
| Seminal vesicle      | 0.0178      |             |        |        |
| Sensory organs       | 0.0118      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               | 0.0000      |             |        |        |

| FETUS               |             | STANDARDIZED/SUBTRACTED |             |
|---------------------|-------------|-------------------------|-------------|
|                     | % frequency | LIBRARIES               | % frequency |
| Development         | 0.0278      | Breast                  | 0.0136      |
| Gastrointestinal    | 0.0139      | Ovary_n                 | 0.0000      |
| Brain               | 0.0000      | Ovary_t                 | 0.0152      |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000      |
| Skin                | 0.0000      | Fetal                   | 0.0052      |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0122      |
| Heart-blood vessels | 0.0391      | Hematopoietic           | 0.0000      |
| Lung                | 0.0000      | Skin-muscle             | 0.0032      |
| Suprarenal gland    | 0.0254      | Testicles               | 0.0000      |
| Kidney              | 0.0000      | Lung                    | 0.0000      |
| Placenta            | 0.0061      | Nerves                  | 0.0060      |
| Prostate            | 0.0000      | Prostate                | 0.0000      |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0077      |
|                     |             | Uterus_n                | 0.0083      |

## Electronic Northern for SEQ. ID NO.: 123

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0390      | 0.0051      | 7.6272 | 0.1311 |
| Breast               | 0.0064      | 0.0056      | 1.1342 | 0.8817 |
| Small intestine      | 0.0184      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0060      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0017      | 0.0050      | 0.3396 | 2.9444 |
| Gastrointestinal     | 0.0057      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0007      | 0.0021      | 0.3600 | 2.7779 |
| Hematopoietic        | 0.0040      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0095      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0000      | 0.0000      | undef  | undef  |
| Lung                 | 0.0021      | 0.0020      | 1.0161 | 0.9842 |
| Stomach-esophagus    | 0.0193      | 0.0077      | 2.5211 | 0.3967 |
| Muscle-skeleton      | 0.0154      | 0.0060      | 2.5700 | 0.3891 |
| Kidney               | 0.0054      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0000      | 0.0055      | 0.0000 | undef  |
| Penis                | 0.0210      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0044      | 0.0000      | undef  | 0.0000 |
| Uterus-endometrium   | 0.0203      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0152      | 0.0272      | 0.5611 | 1.7821 |
| Uterus-general       | 0.0000      | 0.0000      | undef  | undef  |
| Breast hyperplasia   | 0.0128      |             |        |        |
| Prostate hyperplasia | 0.0059      |             |        |        |
| Seminal vesicle      | 0.0000      |             |        |        |
| Sensory organs       | 0.0017      |             |        |        |
| White blood cells    | 0.0000      |             |        |        |
| Cervix               |             |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0139      | Breast                  | 0.0000 |
| Gastrointestinal    | 0.0083      | Ovary_n                 | 0.0000 |
| Brain               | 0.0000      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0000 |
| Skin                | 0.0000      | Fetal                   | 0.0012 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0122 |
| Heart-blood vessels | 0.0142      | Hematopoietic           | 0.0000 |
| Lung                | 0.0000      | Skin-muscle             | 0.0065 |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000 |
| Kidney              | 0.0000      | Lung                    | 0.0082 |
| Placenta            | 0.0000      | Nerves                  | 0.0000 |
| Prostate            | 0.0000      | Prostate                | 0.0000 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0083 |



## Electronic Northern for SEQ. ID NO.: 125

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0390      | 0.0051      | 7.6272 | 0.1311 |
| Breast               | 0.0153      | 0.0150      | 1.0208 | 0.9796 |
| Small intestine      | 0.0245      | 0.0000      | undef  | 0.0000 |
| Ovary                | 0.0210      | 0.0078      | 2.6863 | 0.3723 |
| Endocrine tissue     | 0.0170      | 0.0125      | 1.3585 | 0.7361 |
| Gastrointestinal     | 0.0153      | 0.0000      | undef  | 0.0000 |
| Brain                | 0.0126      | 0.0133      | 0.9415 | 1.0622 |
| Hematopoietic        | 0.0067      | 0.0000      | undef  | 0.0000 |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0129      | 0.0000 | undef  |
| Heart                | 0.0127      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0115      | 0.0117      | 0.9839 | 1.0163 |
| Lung                 | 0.0114      | 0.0143      | 0.7983 | 1.2326 |
| Stomach-esophagus    | 0.0097      | 0.0307      | 0.3151 | 3.1733 |
| Muscle-skeleton      | 0.0034      | 0.0060      | 0.5711 | 1.7510 |
| Kidney               | 0.0326      | 0.0274      | 1.1896 | 0.8406 |
| Pancreas             | 0.0033      | 0.0166      | 0.1994 | 5.0142 |
| Penis                | 0.0629      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0109      | 0.0170      | 0.6398 | 1.5631 |
| Uterus-endometrium   | 0.0203      | 0.0000      | undef  | 0.0000 |
| Uterus-myometrium    | 0.0305      | 0.0068      | 4.4891 | 0.2228 |
| Uterus-general       | 0.0255      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0256      |             |        |        |
| Prostate hyperplasia | 0.0208      |             |        |        |
| Seminal vesicle      | 0.0178      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0191      |             |        |        |
| Cervix               | 0.0106      |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | % frequency             |        |
| Development         | 0.0000      | Breast                  |        |
| Gastrointestinal    | 0.0111      | Ovary_n                 | 0.0000 |
| Brain               | 0.0063      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0000      | Endocrine tissue        | 0.0051 |
| Skin                | 0.0000      | Fetal                   | 0.0000 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0076 |
| Heart-blood vessels | 0.0036      | Hematopoietic           | 0.0000 |
| Lung                | 0.0072      | Skin-muscle             | 0.0057 |
| Suprarenal gland    | 0.0254      | Testicles               | 0.0162 |
| Kidney              | 0.0062      | Lung                    | 0.0077 |
| Placenta            | 0.0000      | Nerves                  | 0.0082 |
| Prostate            | 0.0000      | Nerves                  | 0.0120 |
| Sensory organs      | 0.0126      | Prostate                | 0.0205 |
|                     |             | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0749 |

## Electronic Northern for SEQ. ID NO.: 126

|                      | NORMAL      | TUMOR       | Ratios |         |
|----------------------|-------------|-------------|--------|---------|
|                      | % frequency | % frequency | N/T    | T/N     |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000  |
| Breast               | 0.0051      | 0.0056      | 0.9074 | 1.1021  |
| Small intestine      | 0.0184      | 0.0000      | undef  | 0.0000  |
| Ovary                | 0.0050      | 0.0104      | 0.5756 | 1.7372  |
| Endocrine tissue     | 0.0085      | 0.0075      | 1.1321 | 0.8833  |
| Gastrointestinal     | 0.0096      | 0.0000      | undef  | 0.0000  |
| Brain                | 0.0059      | 0.0154      | 0.3840 | 2.6043  |
| Hematopoietic        | 0.0080      | 0.0000      | undef  | 0.0000  |
| Skin                 | 0.0073      | 0.0000      | undef  | 0.0000  |
| Hepatic              | 0.0095      | 0.0129      | 0.7353 | 1.3600  |
| Heart                | 0.0201      | 0.0137      | 1.4649 | 0.6827  |
| Testicles            | 0.0058      | 0.0000      | undef  | 0.0000  |
| Lung                 | 0.0145      | 0.0164      | 0.8891 | 1.1248  |
| Stomach-esophagus    | 0.0000      | 0.0230      | 0.0000 | undef   |
| Muscle-skeleton      | 0.0017      | 0.0300      | 0.0571 | 17.5100 |
| Kidney               | 0.0217      | 0.0068      | 3.1722 | 0.3152  |
| Pancreas             | 0.0050      | 0.0000      | undef  | 0.0000  |
| Penis                | 0.0210      | 0.0000      | undef  | 0.0000  |
| Prostate             | 0.0065      | 0.0021      | 3.0709 | 0.3256  |
| Uterus-endometrium   | 0.0135      | 0.0000      | undef  | 0.0000  |
| Uterus-myometrium    | 0.0457      | 0.0204      | 2.2445 | 0.4455  |
| Uterus-general       | 0.0153      | 0.0000      | undef  | 0.0000  |
| Breast hyperplasia   | 0.0096      |             |        |         |
| Prostate hyperplasia | 0.0000      |             |        |         |
| Seminal vesicle      | 0.0000      |             |        |         |
| Sensory organs       | 0.0470      |             |        |         |
| White blood cells    | 0.0121      |             |        |         |
| Cervix               | 0.0213      |             |        |         |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |        |
|---------------------|-------------|-------------------------|--------|
|                     | % frequency | LIBRARIES               |        |
|                     |             | % frequency             |        |
| Development         | 0.0139      | Breast                  |        |
| Gastrointestinal    | 0.0056      | Ovary_n                 | 0.0068 |
| Brain               | 0.0000      | Ovary_t                 | 0.0000 |
| Hematopoietic       | 0.0157      | Endocrine tissue        | 0.0101 |
| Skin                | 0.0000      | Fetal                   | 0.0000 |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0210 |
| Heart-blood vessels | 0.0213      | Hematopoietic           | 0.0122 |
| Lung                | 0.0217      | Skin-muscle             | 0.0057 |
| Suprarenal gland    | 0.0254      | Testicles               | 0.0259 |
| Kidney              | 0.0185      | Lung                    | 0.0000 |
| Placenta            | 0.0121      | Nerves                  | 0.0000 |
| Prostate            | 0.0000      | Prostate                | 0.0020 |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000 |
|                     |             | Uterus_n                | 0.0387 |
|                     |             |                         | 0.0000 |



## Electronic Northern for SEQ. ID NO.: 127

|                      | NORMAL      | TUMOR       | Ratios |        |
|----------------------|-------------|-------------|--------|--------|
|                      | % frequency | % frequency | N/T    | T/N    |
| Bladder              | 0.0156      | 0.0000      | undef  | 0.0000 |
| Breast               | 0.0090      | 0.0019      | 4.7637 | 0.2099 |
| Small intestine      | 0.0000      | 0.0000      | undef  | undef  |
| Ovary                | 0.0240      | 0.0000      | undef  | 0.0000 |
| Endocrine tissue     | 0.0017      | 0.0025      | 0.6792 | 1.4722 |
| Gastrointestinal     | 0.0000      | 0.0046      | 0.0000 | undef  |
| Brain                | 0.0037      | 0.0010      | 3.5998 | 0.2779 |
| Hematopoietic        | 0.0000      | 0.0000      | undef  | undef  |
| Skin                 | 0.0037      | 0.0000      | undef  | 0.0000 |
| Hepatic              | 0.0000      | 0.0000      | undef  | undef  |
| Heart                | 0.0074      | 0.0000      | undef  | 0.0000 |
| Testicles            | 0.0058      | 0.0234      | 0.2460 | 4.0652 |
| Lung                 | 0.0010      | 0.0061      | 0.1693 | 5.9051 |
| Stomach-esophagus    | 0.0000      | 0.0000      | undef  | undef  |
| Muscle-skeleton      | 0.0000      | 0.0060      | 0.0000 | undef  |
| Kidney               | 0.0027      | 0.0000      | undef  | 0.0000 |
| Pancreas             | 0.0017      | 0.0110      | 0.1496 | 6.6857 |
| Penis                | 0.0090      | 0.0000      | undef  | 0.0000 |
| Prostate             | 0.0044      | 0.0064      | 0.6824 | 1.4654 |
| Uterus-endometrium   | 0.0000      | 0.0000      | undef  | undef  |
| Uterus-myometrium    | 0.0223      | 0.0136      | 1.6834 | 0.5940 |
| Uterus-general       | 0.0102      | 0.0000      | undef  | 0.0000 |
| Breast hyperplasia   | 0.0032      |             |        |        |
| Prostate hyperplasia | 0.0119      |             |        |        |
| Seminal vesicle      | 0.0267      |             |        |        |
| Sensory organs       | 0.0000      |             |        |        |
| White blood cells    | 0.0017      |             |        |        |
| Cervix               | 0.0000      |             |        |        |

|                     | FETUS       | STANDARDIZED/SUBTRACTED |             |
|---------------------|-------------|-------------------------|-------------|
|                     | % frequency | LIBRARIES               | % frequency |
| Development         | 0.0139      | Breast                  | 0.0000      |
| Gastrointestinal    | 0.0000      | Ovary_n                 | 0.0000      |
| Brain               | 0.0000      | Ovary_t                 | 0.0000      |
| Hematopoietic       | 0.0079      | Endocrine tissue        | 0.0000      |
| Skin                | 0.0000      | Fetal                   | 0.0000      |
| Hepatic             | 0.0000      | Gastrointestinal        | 0.0122      |
| Heart-blood vessels | 0.0071      | Hematopoietic           | 0.0000      |
| Lung                | 0.0036      | Skin-muscle             | 0.0000      |
| Suprarenal gland    | 0.0000      | Testicles               | 0.0000      |
| Kidney              | 0.0000      | Lung                    | 0.0092      |
| Placenta            | 0.0000      | Nerves                  | 0.0010      |
| Prostate            | 0.0000      | Prostate                | 0.0205      |
| Sensory organs      | 0.0000      | Sensory Organs          | 0.0000      |
|                     |             | Uterus_n                | 0.0042      |

## Electronic Northern for Seq. ID: 391

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0025            | 0.0000           | undef 0.0000      |
| Bladder           | 0.0312            | 0.0000           | undef 0.0000      |
| Breast            | 0.0079            | 0.0056           | 1.4090 0.7097     |
| Large intestine   | 0.0077            | 0.0000           | undef 0.0000      |
| Small intestine   | 0.0027            | 0.0107           | 0.2577 1.8812     |
| Ovary             | 0.0030            | 0.0072           | 0.4148 2.4109     |
| Endocrine tissue  | 0.0048            | 0.0089           | 0.5432 1.8409     |
| Brain             | 0.0029            | 0.0080           | 0.3627 2.7574     |
| Skin              | 0.0000            | 0.0000           | undef undef       |
| Hepatic           | 0.0093            | 0.0000           | undef 0.0000      |
| Heart             | 0.0020            | 0.0000           | undef 0.0000      |
| Testicles         | 0.0000            | 0.0118           | 0.0000 undef      |
| Lung              | 0.0010            | 0.0037           | 0.2631 1.8007     |
| Stomach-esophagus | 0.0217            | 0.0000           | undef 0.0000      |
| Muscle-skeleton   | 0.0034            | 0.0000           | undef 0.0000      |
| Kidney            | 0.0045            | 0.0048           | 0.9285 1.0770     |
| Pancreas          | 0.0017            | 0.0055           | 0.2992 3.3427     |
| Prostate          | 0.0066            | 0.0039           | 1.6882 0.5923     |
| T lymphoma        | 0.0025            | 0.0149           | 0.1691 5.9152     |
| Uterus            | 0.0030            | 0.0046           | 0.6426 1.5563     |
| White blood cells | 0.0021            | 0.0000           | undef 0.0000      |
| Hematopoietic     | 0.0000            |                  |                   |
| Penis             | 0.0134            |                  |                   |
| Seminal vesicle   | 0.0070            |                  |                   |
| Sensory organs    | 0.0000            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0278 |
| Gastrointestinal    | 0.0000 |
| Brain               | 0.0188 |
| Hematopoietic       | 0.0079 |
| Skin                | 0.0000 |
| Hepatic             | 0.0260 |
| Heart-blood vessels | 0.0071 |
| Lung                | 0.0000 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0000 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0126 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0000 |
| Breast_t          | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0245 |
| Gastrointestinal  | 0.0064 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0000 |
| Testicles_n       | 0.0065 |
| Testicles_t       | 0.0157 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0000 |
| Nerves            | 0.0000 |
| Kidney_t          | 0.0060 |
| Ovary uterus      | 0.0000 |
| Prostate_n        | 0.0090 |
| Sensory organs    | 0.0132 |
| White blood cells | 0.0000 |
|                   | 0.0000 |

Electronic Northern for Seq. ID: 392

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0000            | 0.0000           | undef undef       |
| Bladder           | 0.0156            | 0.0000           | undef 0.0000      |
| Breast            | 0.0000            | 0.0000           | undef undef       |
| Large intestine   | 0.0000            | 0.0000           | undef undef       |
| Small intestine   | 0.0000            | 0.0000           | undef undef       |
| Ovary             | 0.0059            | 0.0000           | undef 0.0000      |
| Endocrine tissue  | 0.0000            | 0.0000           | undef undef       |
| Brain             | 0.0000            | 0.0000           | undef undef       |
| Skin              | 0.0000            | 0.0000           | undef undef       |
| Hepatic           | 0.0000            | 0.0000           | undef undef       |
| Heart             | 0.0000            | 0.0000           | undef undef       |
| Testicles         | 0.0010            | 0.0000           | undef 0.0000      |
| Lung              | 0.0000            | 0.0000           | undef undef       |
| Stomach-esophagus | 0.0000            | 0.0000           | undef undef       |
| Muscle-skeleton   | 0.0000            | 0.0000           | undef undef       |
| Kidney            | 0.0000            | 0.0000           | undef undef       |
| Pancreas          | 0.0000            | 0.0000           | undef undef       |
| Prostate          | 0.0000            | 0.0000           | undef undef       |
| T lymphoma        | 0.0000            | 0.0000           | undef undef       |
| Uterus            | 0.0000            | 0.0000           | undef undef       |
| White blood cells | 0.0000            | 0.0000           | undef undef       |
| Hematopoietic     | 0.0000            |                  |                   |
| Penis             | 0.0000            |                  |                   |
| Seminal vesicle   | 0.0000            |                  |                   |
| Sensory organs    | 0.0000            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0000 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0000 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung                | 0.0000 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0000 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0000 |
| Breast_t          | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0000 |
| Gastrointestinal  | 0.0000 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0000 |
| Testicles_n       | 0.0000 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0000 |
| Nerves            | 0.0010 |
| Kidney_t          | 0.0000 |
| Ovary uterus      | 0.0023 |
| Prostate_n        | 0.0000 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0000 |

## Electronic Northern for Seq. ID: 393

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0075            | 0.0000           | undef 0.0000      |
| Bladder           | 0.0195            | 0.0000           | undef 0.0000      |
| Breast            | 0.0009            | 0.0000           | undef 0.0000      |
| Large intestine   | 0.0037            | 0.0000           | undef 0.0000      |
| Small intestine   | 0.0000            | 0.0000           | undef undef       |
| Ovary             | 0.0000            | 0.0000           | undef undef       |
| Endocrine tissue  | 0.0000            | 0.0000           | undef undef       |
| Brain             | 0.0000            | 0.0000           | undef undef       |
| Skin              | 0.0000            | 0.0000           | undef undef       |
| Hepatic           | 0.0000            | 0.0000           | undef undef       |
| Heart             | 0.0046            | 0.0000           | undef 0.0000      |
| Testicles         | 0.0000            | 0.0000           | undef undef       |
| Lung              | 0.0000            | 0.0000           | undef undef       |
| Stomach-esophagus | 0.0010            | 0.0000           | undef 0.0000      |
| Muscle-skeleton   | 0.0000            | 0.0000           | undef undef       |
| Kidney            | 0.0034            | 0.0000           | undef 0.0000      |
| Pancreas          | 0.0000            | 0.0000           | undef undef       |
| Prostate          | 0.0000            | 0.0055           | 0.0000 undef      |
| T lymphoma        | 0.0000            | 0.0000           | undef undef       |
| Uterus            | 0.0000            | 0.0000           | undef undef       |
| White blood cells | 0.0000            | 0.0000           | undef undef       |
| Hematopoietic     | 0.0000            | 0.0000           | undef undef       |
| Penis             | 0.0027            |                  |                   |
| Seminal vesicle   | 0.0000            |                  |                   |
| Sensory organs    | 0.0000            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0000 |
| Brain               | 0.0063 |
| Hematopoietic       | 0.0039 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung                | 0.0000 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0000 |
| Placenta            | 0.0061 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0000 |
| Breast t          | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0029 |
| Gastrointestinal  | 0.0000 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0000 |
| Testicles_n       | 0.0042 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0000 |
| Nerves            | 0.0020 |
| Kidney t          | 0.0000 |
| Ovary Uterus      | 0.0045 |
| Prostate_n        | 0.0000 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0000 |

## Electronic Northern for Seq. ID: 394

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0000            | 0.0136           | 0.0000 undef      |
| Bladder           | 0.0156            | 0.0023           | 6.6380 0.1506     |
| Breast            | 0.0035            | 0.0042           | 0.8349 1.1977     |
| Large intestine   | 0.0038            | 0.0199           | 0.1922 5.2023     |
| Small intestine   | 0.0000            | 0.0000           | undef undef       |
| Ovary             | 0.0059            | 0.0024           | 2.4887 0.4018     |
| Endocrine tissue  | 0.0080            | 0.0000           | undef 0.0000      |
| Brain             | 0.0023            | 0.0040           | 0.5803 1.7234     |
| Skin              | 0.0073            | 0.0000           | undef 0.0000      |
| Hepatic           | 0.0000            | 0.0000           | undef undef       |
| Heart             | 0.0030            | 0.0000           | undef 0.0000      |
| Testicles         | 0.0000            | 0.0059           | 0.0000 undef      |
| Lung              | 0.0013            | 0.0053           | 0.3508 2.8506     |
| Stomach-esophagus | 0.0072            | 0.0000           | undef 0.0000      |
| Muscle-skeleton   | 0.0017            | 0.0000           | undef 0.0000      |
| Kidney            | 0.0045            | 0.0048           | 0.9285 1.0770     |
| Pancreas          | 0.0033            | 0.0110           | 0.2992 3.3427     |
| Prostate          | 0.0057            | 0.0026           | 2.1706 0.4607     |
| T lymphoma        | 0.0051            | 0.0149           | 0.3381 2.5576     |
| Uterus            | 0.0015            | 0.0000           | undef 0.0000      |
| White blood cells | 0.0021            | 0.0304           | 0.0676 14.7861    |
| Hematopoietic     | 0.0013            |                  |                   |
| Penis             | 0.0054            |                  |                   |
| Seminal vesicle   | 0.0000            |                  |                   |
| Sensory organs    | 0.0118            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0028 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0000 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung                | 0.0036 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0062 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            |        |
| Breast_t          | 0.0136 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0051 |
| Fetal             | 0.0000 |
| Gastrointestinal  | 0.0017 |
| Hematopoietic     | 0.0122 |
| Skin-muscle       | 0.0000 |
| Testicles_n       | 0.0000 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0293 |
| Nerves            | 0.0000 |
| Kidney_t          | 0.0040 |
| Ovary uterus      | 0.0000 |
| Prostate_n        | 0.0068 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0000 |
|                   | 0.0000 |

## Electronic Northern for Seq. ID: 395

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0000            | 0.0000           | undef undef       |
| Bladder           | 0.0156            | 0.0047           | 3.3192 0.3013     |
| Breast            | 0.0062            | 0.0183           | 0.3372 2.9657     |
| Large intestine   | 0.0019            | 0.0114           | 0.1682 5.9454     |
| Small intestine   | 0.0000            | 0.0107           | 0.0000 undef      |
| Ovary             | 0.0030            | 0.0072           | 0.4148 2.4110     |
| Endocrine tissue  | 0.0000            | 0.0000           | undef undef       |
| Brain             | 0.0006            | 0.0010           | 0.6045 1.6542     |
| Hepatic           | 0.0073            | 0.0000           | undef 0.0000      |
| Heart             | 0.0000            | 0.0190           | 0.0000 undef      |
| Testicles         | 0.0020            | 0.0962           | 0.0211 47.4018    |
| Lung              | 0.0000            | 0.0000           | undef undef       |
| Stomach-esophagus | 0.0039            | 0.0111           | 0.3508 2.8506     |
| Muscle-skeleton   | 0.0000            | 0.0000           | undef undef       |
| Kidney            | 0.0171            | 0.0037           | 4.6389 0.2156     |
| Pancreas          | 0.0043            | 0.0000           | undef 0.0000      |
| Prostate          | 0.0000            | 0.0110           | 0.0000 undef      |
| T lymphoma        | 0.0000            | 0.0052           | 0.0000 undef      |
| Uterus            | 0.0025            | 0.0000           | undef 0.0000      |
| White blood cells | 0.0015            | 0.0000           | undef 0.0000      |
| Hematopoietic     | 0.0000            | 0.0000           | undef undef       |
| Penis             | 0.0013            |                  |                   |
| Seminal vesicle   | 0.0054            |                  |                   |
| Sensory organs    | 0.0000            |                  |                   |
|                   | 0.0000            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0278 |
| Gastrointestinal    | 0.0056 |
| Brain               | 0.0063 |
| Hematopoietic       | 0.0000 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0071 |
| Lung                | 0.0000 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0000 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0000 |
| Breast_t          | 0.0000 |
| Large Intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0152 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0006 |
| Gastrointestinal  | 0.0000 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0000 |
| Testicles_n       | 0.0000 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0000 |
| Nerves            | 0.0000 |
| Kidney_t          | 0.0000 |
| Ovary uterus      | 0.0113 |
| Prostate_n        | 0.0000 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0000 |

## Electronic Northern for Seq. ID: 396

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0000            | 0.0136           | 0.0000 undef      |
| Bladder           | 0.0429            | 0.0000           | undef 0.0000      |
| Breast            | 0.0000            | 0.0042           | 0.0000 undef      |
| Large intestine   | 0.0038            | 0.0000           | undef 0.0000      |
| Small intestine   | 0.0000            | 0.0000           | undef undef       |
| Ovary             | 0.0000            | 0.0000           | undef undef       |
| Endocrine tissue  | 0.0000            | 0.0000           | undef undef       |
| Brain             | 0.0032            | 0.0000           | undef 0.0000      |
| Skin              | 0.0012            | 0.0010           | 1.1605 0.8617     |
| Hepatic           | 0.0037            | 0.0000           | undef 0.0000      |
| Heart             | 0.0046            | 0.0000           | undef 0.0000      |
| Testicles         | 0.0051            | 0.0000           | undef 0.0000      |
| Lung              | 0.0000            | 0.0000           | undef undef       |
| Stomach-esophagus | 0.0000            | 0.0055           | 0.0000 undef      |
| Muscle-skeleton   | 0.0000            | 0.0064           | 0.0000 undef      |
| Kidney            | 0.0017            | 0.0037           | 0.4639 2.1557     |
| Pancreas          | 0.0045            | 0.0000           | undef 0.0000      |
| Prostate          | 0.0017            | 0.0000           | undef 0.0000      |
| T lymphoma        | 0.0009            | 0.0026           | 0.3618 2.7643     |
| Uterus            | 0.0000            | 0.0000           | undef undef       |
| White blood cells | 0.0030            | 0.0000           | undef 0.0000      |
| Hematopoietic     | 0.0007            | 0.0000           | undef 0.0000      |
| Penis             | 0.0000            |                  |                   |
| Seminal vesicle   | 0.0054            |                  |                   |
| Sensory organs    | 0.0000            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0000 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0000 |
| Skin                | 0.0000 |
| Hepatic             | 0.0036 |
| Heart-blood vessels | 0.0000 |
| Lung                | 0.0000 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0000 |
| Placenta            | 0.0249 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            |        |
| Breast_t          | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0000 |
| Gastrointestinal  | 0.0075 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0000 |
| Testicles_n       | 0.0000 |
| Testicles_t       | 0.0084 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0098 |
| Nerves            | 0.0000 |
| Kidney_t          | 0.0070 |
| Ovary uterus      | 0.0000 |
| Prostate_n        | 0.0000 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0077 |
|                   | 0.0000 |

## Electronic Northern for Seq. ID: 397

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0025            | 0.0000           | undef 0.0000      |
| Bladder           | 0.0117            | 0.0000           | undef 0.0000      |
| Breast            | 0.0009            | 0.0000           | undef 0.0000      |
| Large intestine   | 0.0000            | 0.0000           | undef undef       |
| Small intestine   | 0.0000            | 0.0000           | undef undef       |
| Ovary             | 0.0030            | 0.0000           | undef 0.0000      |
| Endocrine tissue  | 0.0048            | 0.0000           | undef 0.0000      |
| Brain             | 0.0006            | 0.0000           | undef 0.0000      |
| Skin              | 0.0000            | 0.0000           | undef undef       |
| Hepatic           | 0.0000            | 0.0063           | 0.0000 undef      |
| Heart             | 0.0010            | 0.0000           | undef 0.0000      |
| Testicles         | 0.0000            | 0.0000           | undef undef       |
| Lung              | 0.0019            | 0.0018           | 1.0524 0.9502     |
| Stomach-esophagus | 0.0000            | 0.0000           | undef undef       |
| Muscle-skeleton   | 0.0000            | 0.0000           | undef undef       |
| Kidney            | 0.0000            | 0.0000           | undef undef       |
| Pancreas          | 0.0000            | 0.0000           | undef undef       |
| Prostate          | 0.0009            | 0.0026           | 0.3618 2.7643     |
| T lymphoma        | 0.0000            | 0.0000           | undef undef       |
| Uterus            | 0.0000            | 0.0000           | undef undef       |
| White blood cells | 0.0007            | 0.0000           | undef 0.0000      |
| Hematopoietic     | 0.0000            |                  |                   |
| Penis             | 0.0000            |                  |                   |
| Seminal vesicle   | 0.0000            |                  |                   |
| Sensory organs    | 0.0000            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0028 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0039 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung                | 0.0000 |
| Adrenal gland       | 0.0062 |
| Kidney              | 0.0000 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0068 |
| Breast_t          | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0051 |
| Fetal             | 0.0000 |
| Gastrointestinal  | 0.0070 |
| Hematopoietic     | 0.0122 |
| Skin-muscle       | 0.0000 |
| Testicles_n       | 0.0293 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0000 |
| Nerve_s           | 0.0000 |
| Kidney_t          | 0.0000 |
| Ovary uterus      | 0.0135 |
| Prostate_n        | 0.0061 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0000 |



## Electronic Northern for Seq. ID: 398

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0023            | 0.0000           | undef 0.0000      |
| Bladder           | 0.0156            | 0.0023           | 6.6384 0.1306     |
| Breast            | 0.0033            | 0.0042           | 1.2524 0.7985     |
| Large intestine   | 0.0000            | 0.0028           | 0.0000 undef      |
| Small intestine   | 0.0027            | 0.0000           | undef 0.0000      |
| Ovary             | 0.0030            | 0.0024           | 1.2443 0.8037     |
| Endocrine tissue  | 0.0000            | 0.0037           | 0.0000 undef      |
| Brain             | 0.0024            | 0.0060           | 0.4030 2.4814     |
| Skin              | 0.0000            | 0.0000           | undef undef       |
| Hepatic           | 0.0000            | 0.0000           | undef undef       |
| Heart             | 0.0030            | 0.0137           | 0.2213 4.5145     |
| Testicles         | 0.0080            | 0.0000           | undef 0.0000      |
| Lung              | 0.0068            | 0.0037           | 1.8417 0.5430     |
| Stomach-esophagus | 0.0000            | 0.0000           | undef undef       |
| Muscle-skeleton   | 0.0034            | 0.0000           | undef 0.0000      |
| Kidney            | 0.0022            | 0.0000           | undef 0.0000      |
| Pancreas          | 0.0000            | 0.0055           | 0.0000 undef      |
| Prostate          | 0.0028            | 0.0026           | 1.0853 0.9214     |
| T lymphoma        | 0.0000            | 0.0000           | undef undef       |
| Uterus            | 0.0000            | 0.0092           | 0.0000 undef      |
| White blood cells | 0.0082            | 0.0000           | undef 0.0000      |
| Hematopoietic     | 0.0013            |                  |                   |
| Penis             | 0.0054            |                  |                   |
| Seminal vesicle   | 0.0070            |                  |                   |
| Sensory organs    | 0.0000            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0028 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0000 |
| Skin                | 0.0000 |
| Hepatic             | 0.0036 |
| Heart-blood vessels | 0.0000 |
| Lung                | 0.0000 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0000 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0068 |
| Breast_t          | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0006 |
| Gastrointestinal  | 0.0122 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0065 |
| Testicles_n       | 0.0000 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0000 |
| Nerves            | 0.0030 |
| Kidney_t          | 3.0000 |
| Ovary uterus      | 0.0090 |
| Prostate_n        | 0.0000 |
| Sensory organs    | 2.0000 |
| White blood cells | 0.0000 |

## Electronic Northern for Seq. ID: 399

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0000            | 0.0136           | 0.0000 undef      |
| Bladder           | 0.0234            | 0.0047           | 4.9788 0.2009     |
| Breast            | 0.0070            | 0.0098           | 0.7157 1.3973     |
| Large intestine   | 0.0057            | 0.0085           | 0.6728 1.4864     |
| Small intestine   | 0.0110            | 0.0000           | undef 0.0000      |
| Ovary             | 0.0059            | 0.0000           | undef 0.0000      |
| Endocrine tissue  | 0.0032            | 0.0038           | 0.8479 1.1794     |
| Brain             | 0.0018            | 0.0020           | 0.9068 1.1028     |
| Skin              | 0.0073            | 0.0000           | undef 0.0000      |
| Hepatic           | 0.0046            | 0.0190           | 0.2441 4.0960     |
| Heart             | 0.0081            | 0.0000           | undef 0.0000      |
| Testicles         | 0.0040            | 0.0000           | undef 0.0000      |
| Lung              | 0.0068            | 0.0018           | 3.6834 0.2715     |
| Stomach-esophagus | 0.0072            | 0.0064           | 1.1333 0.8824     |
| Muscle-skeleton   | 0.0069            | 0.0000           | undef 0.0000      |
| Kidney            | 0.0067            | 0.0096           | 0.6963 1.4362     |
| Pancreas          | 0.0033            | 0.0221           | 0.1496 6.6857     |
| Prostate          | 0.0094            | 0.0052           | 1.8088 0.5529     |
| T lymphoma        | 0.0000            | 0.0000           | undef undef       |
| Uterus            | 0.0093            | 0.0000           | undef 0.0000      |
| White blood cells | 0.0068            | 0.0000           | undef 0.0000      |
| Hematopoietic     | 0.0000            |                  |                   |
| Penis             | 0.0134            |                  |                   |
| Seminal vesicle   | 0.0070            |                  |                   |
| Sensory organs    | 0.0118            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0139 |
| Gastrointestinal    | 0.0111 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0000 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung                | 0.0145 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0000 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0408 |
| Breast_t          | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.1595 |
| Endocrine tissue  | 0.0101 |
| Fetal             | 0.0000 |
| Gastrointestinal  | 0.0046 |
| Hematopoietic     | 0.0122 |
| Skin-muscle       | 0.0000 |
| Testicles_n       | 0.0130 |
| Testicles_t       | 0.0125 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0098 |
| Nerves            | 0.0000 |
| Kidney_t          | 0.0000 |
| Ovary uterus      | 0.0000 |
| Prostate_n        | 0.0068 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 400

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0000            | 0.0136           | 0.0000 undef      |
| Bladder           | 0.0156            | 0.0000           | undef 0.0000      |
| Breast            | 0.0018            | 0.0000           | undef 0.0000      |
| Large intestine   | 0.0000            | 0.0000           | undef undef       |
| Small intestine   | 0.0000            | 0.0000           | undef undef       |
| Ovary             | 0.0000            | 0.0000           | undef undef       |
| Endocrine tissue  | 0.0000            | 0.0000           | undef undef       |
| Brain             | 0.0015            | 0.0019           | 0.8473 1.1794     |
| Skin              | 0.0018            | 0.0010           | 1.8135 0.5514     |
| Hepatic           | 0.0073            | 0.0000           | undef 0.0000      |
| Heart             | 0.0046            | 0.0000           | undef 0.0000      |
| Testicles         | 0.0020            | 0.0000           | undef 0.0000      |
| Lung              | 0.0040            | 0.0000           | undef 0.0000      |
| Stomach-esophagus | 0.0000            | 0.0000           | undef undef       |
| Muscle-skeleton   | 0.0000            | 0.0000           | undef undef       |
| Kidney            | 0.0000            | 0.0000           | undef undef       |
| Pancreas          | 0.0033            | 0.0000           | undef 0.0000      |
| Prostate          | 0.0047            | 0.0026           | 1.8089 0.5529     |
| T lymphoma        | 0.0025            | 0.0000           | undef 0.0000      |
| Uterus            | 0.0031            | 0.0000           | undef 0.0000      |
| White blood cells | 0.0000            | 0.0000           | undef undef       |
| Hematopoietic     | 0.0000            | 0.0000           | undef undef       |
| Penis             | 0.0027            |                  |                   |
| Seminal vesicle   | 0.0000            |                  |                   |
| Sensory organs    | 0.0000            |                  |                   |

# FETUS % freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0000 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0039 |
| Skin                | 0.0000 |
| Hepatic             | 0.0260 |
| Heart-blood vessels | 0.0000 |
| Lung                | 0.0000 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0000 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

# STANDARDIZED/SUBTRACTED LIBRARIES % frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0204 |
| Breast_t          | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0110 |
| Gastrointestinal  | 0.0000 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0000 |
| Testicles_n       | 0.0000 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0000 |
| Nerves            | 0.0040 |
| Kidney_t          | 0.0000 |
| Ovary uterus      | 0.0045 |
| Prostate_n        | 0.0121 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0000 |

Electronic Northern for Seq. ID: 401

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0125            | 0.0136           | 0.9198 1.0872     |
| Bladder           | 0.0390            | 0.0094           | 4.1487 0.2410     |
| Breast            | 0.0158            | 0.0056           | 2.8179 0.3549     |
| Large intestine   | 0.0172            | 0.0028           | 6.0551 0.1652     |
| Small intestine   | 0.0110            | 0.0000           | undef 0.0000      |
| Ovary             | 0.0178            | 0.0119           | 1.4932 0.6697     |
| Endocrine tissue  | 0.0161            | 0.0195           | 0.8231 1.2150     |
| Brain             | 0.0179            | 0.0170           | 1.0581 0.9451     |
| Skin              | 0.0220            | 0.0000           | undef 0.0000      |
| Hepatic           | 0.0000            | 0.0000           | undef undef       |
| Heart             | 0.0162            | 0.0275           | 0.5907 1.6929     |
| Testicles         | 0.0161            | 0.0000           | undef 0.0000      |
| Lung              | 0.0175            | 0.0092           | 1.8944 0.5279     |
| Stomach-esophagus | 0.0000            | 0.0128           | 0.0000 undef      |
| Muscle-skeleton   | 0.0257            | 0.0037           | 6.9583 0.1437     |
| Kidney            | 0.0201            | 0.0096           | 2.0891 0.4787     |
| Pancreas          | 0.0066            | 0.0276           | 0.2393 4.1784     |
| Prostate          | 0.0104            | 0.0000           | undef 0.0000      |
| T lymphoma        | 0.0051            | 0.0448           | 0.1127 8.9727     |
| Uterus            | 0.0177            | 0.0776           | 0.5426 1.5563     |
| White blood cells | 0.0116            | 0.0407           | 0.1916 5.2186     |
| Hematopoietic     | 0.0040            |                  |                   |
| Penis             | 0.0241            |                  |                   |
| Seminal vesicle   | 0.0070            |                  |                   |
| Sensory organs    | 0.0353            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0056 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0157 |
| Skin                | 0.0000 |
| Hepatic             | 0.0260 |
| Heart-blood vessels | 0.0036 |
| Lung                | 0.0000 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0185 |
| Placenta            | 0.1212 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0377 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0204 |
| Breast_t          | 0.0000 |
| Large_intestine_t | 0.0000 |
| Ovary_n           | 0.1595 |
| Ovary_t           | 0.0253 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0226 |
| Gastrointestinal  | 0.0122 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0324 |
| Testicles_n       | 0.0167 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0000 |
| Lungs_t           | 0.0000 |
| Nerves            | 0.0191 |
| Kidney_t          | 0.0000 |
| Ovary Uterus      | 0.0248 |
| Prostate_n        | 0.0061 |
| Sensory organs    | 0.0077 |
| White blood cells | 0.0000 |

## Electronic Northern for Seq. ID: 402

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0125            | 0.0000           | undef 0.0000      |
| Bladder           | 0.0429            | 0.0141           | 3.0424 0.3287     |
| Breast            | 0.0387            | 0.0084           | 4.5922 0.2178     |
| Large intestine   | 0.0038            | 0.0028           | 1.3456 0.7432     |
| Small intestine   | 0.0165            | 0.0107           | 1.5459 0.6469     |
| Ovary             | 0.0237            | 0.0000           | undef 0.0000      |
| Endocrine tissue  | 0.0177            | 0.0018           | 9.9589 0.1004     |
| Brain             | 0.0041            | 0.0100           | 0.4062 2.4620     |
| Skin              | 0.0514            | 0.0000           | undef 0.0000      |
| Hepatic           | 0.0000            | 0.0063           | 0.0000 undef      |
| Heart             | 0.0457            | 0.0137           | 3.3227 0.3010     |
| Testicles         | 0.0040            | 0.0000           | undef 0.0000      |
| Lung              | 0.0467            | 0.0296           | 1.5786 0.6335     |
| Stomach-esophagus | 0.0145            | 0.0064           | 2.2671 0.4411     |
| Muscle-skeleton   | 0.0171            | 0.0222           | 0.7731 1.2934     |
| Kidney            | 0.0000            | 0.0000           | undef undef       |
| Pancreas          | 0.0017            | 0.0000           | undef 0.0000      |
| Prostate          | 0.0075            | 0.0052           | 1.4470 0.6911     |
| T lymphoma        | 0.0051            | 0.0000           | undef 0.0000      |
| Uterus            | 0.0281            | 0.0138           | 2.0348 0.4915     |
| White blood cells | 0.0000            | 0.0000           | undef undef       |
| Hematopoietic     | 0.0160            |                  |                   |
| Penis             | 0.0293            |                  |                   |
| Seminal vesicle   | 0.0141            |                  |                   |
| Sensory organs    | 0.0353            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0418 |
| Gastrointestinal    | 0.0139 |
| Brain               | 0.0000 |
| Hematopoietic       | 0.0039 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0356 |
| Lung                | 0.0325 |
| Adrenal gland       | 0.0000 |
| Kidney              | 0.0124 |
| Placenta            | 0.0121 |
| Prostate            | 0.0249 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0476 |
| Breast_t          | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.1595 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0220 |
| Gastrointestinal  | 0.0122 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0583 |
| Testicles_n       | 0.0042 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0098 |
| Lungs_t           | 0.0000 |
| Nerves            | 0.0090 |
| Kidney_t          | 0.0000 |
| Ovary uterus      | 0.0405 |
| Prostate_n        | 0.0061 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0000 |

## Electronic Northern for Seq. ID: 403

|                   | NORMAL<br>% freq. | TUMOR<br>% freq. | RATIOS<br>N/T T/N |
|-------------------|-------------------|------------------|-------------------|
| B lymphoma        | 0.0000            | 0.0000           | undef undef       |
| Bladder           | 0.0351            | 0.0047           | 7.4677 0.1339     |
| Breast            | 0.0070            | 0.0014           | 5.0097 0.1396     |
| Large intestine   | 0.0115            | 0.0000           | undef 0.0000      |
| Small intestine   | 0.0000            | 0.0000           | undef undef       |
| Ovary             | 0.0000            | 0.0024           | 0.0000 undef      |
| Endocrine tissue  | 0.0016            | 0.0035           | 0.4527 2.2091     |
| Brain             | 0.0017            | 0.0060           | 0.2901 3.4467     |
| Skin              | 0.0000            | 0.0000           | undef undef       |
| Hepatic           | 0.0000            | 0.0063           | 0.0000 undef      |
| Heart             | 0.0020            | 0.0137           | 0.1477 6.7715     |
| Testicles         | 0.0040            | 0.0000           | undef 0.0000      |
| Lung              | 0.0039            | 0.0013           | 2.1049 0.4751     |
| Stomach-esophagus | 0.0145            | 0.0000           | undef 0.0000      |
| Muscle-skeleton   | 0.0051            | 0.0000           | undef 0.0000      |
| Kidney            | 0.0112            | 0.0000           | undef 0.0000      |
| Pancreas          | 0.0017            | 0.0055           | 0.2992 3.3427     |
| Prostate          | 0.0075            | 0.0026           | 2.8941 0.3455     |
| T lymphoma        | 0.0025            | 0.0000           | undef 0.0000      |
| Uterus            | 0.0059            | 0.0046           | 1.2851 0.7781     |
| White blood cells | 0.0027            | 0.0000           | undef 0.0000      |
| Hematopoietic     | 0.0013            |                  |                   |
| Penis             | 0.0054            |                  |                   |
| Seminal vesicle   | 0.0000            |                  |                   |
| Sensory organs    | 0.0000            |                  |                   |

FETUS  
% freq.

|                     |        |
|---------------------|--------|
| Development         | 0.0000 |
| Gastrointestinal    | 0.0000 |
| Brain               | 0.0039 |
| Hematopoietic       | 0.0000 |
| Skin                | 0.0000 |
| Hepatic             | 0.0000 |
| Heart-blood vessels | 0.0000 |
| Lung                | 0.0254 |
| Adrenal gland       | 0.0185 |
| Kidney              | 0.0121 |
| Placenta            | 0.0000 |
| Prostate            | 0.0000 |
| Sensory organs      | 0.0000 |

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

|                   |        |
|-------------------|--------|
| Breast            | 0.0340 |
| Breast_t          | 0.0000 |
| Large intestine_t | 0.0000 |
| Ovary_n           | 0.0000 |
| Ovary_t           | 0.0000 |
| Endocrine tissue  | 0.0000 |
| Fetal             | 0.0017 |
| Gastrointestinal  | 0.0000 |
| Hematopoietic     | 0.0000 |
| Skin-muscle       | 0.0065 |
| Testicles_n       | 0.0000 |
| Testicles_t       | 0.0000 |
| Lungs_n           | 0.0098 |
| Lungs_t           | 0.0000 |
| Nerves            | 0.0020 |
| Kidney_t          | 0.0000 |
| Ovary uterus      | 0.0000 |
| Prostate_n        | 0.0061 |
| Sensory organs    | 0.0000 |
| White blood cells | 0.0000 |

## 2.2. Fisher Test

In order to decide whether a partial sequence  $S$  of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to  $S$ . If the null hypothesis can be rejected with high enough certainty, the gene belonging to  $S$  is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Example 3

#### Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence  $S$  is completed in three steps:

1. Determination of all sequences homologous to  $S$  from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence  $C$  from the assembled sequences.

Consensus sequence  $C$  will generally be longer than initial sequence  $S$ . Its electronic Northern Blot will accordingly

deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences  $C_i$  ( $i$ : iteration index) obtained in each case until the alternative hypothesis is rejected (if  $H_0$  Exit; truncation criterion I) or until automatic lengthening is no longer possible (while  $C_i > C_{i-1}$ ; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from normal bladder tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.



#### Example 4

##### Mapping of Nucleic Acid Sequences on the Human Genome

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

### Example 5

#### Obtaining genomic DNA sequences (BAC clones)

The genomic BAC clones containing the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well". In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

| Seq. ID No. | Identified BACs |          |          |
|-------------|-----------------|----------|----------|
| 60          | 311/K/13        | 271/E/3  | 252/P/20 |
| 102         | 458/N/24        | 349/F/12 |          |

TABLE I

Col. 1 - Sequence ID

Col. 2 - Expression

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Cytogenetic localization

Col. 6 - Nearest marker

TABLE I

| Sequence ID | Expression                             | Function  |
|-------------|--|---|
| 1           | Overexpressed in normal bladder tissue | H. sapiens rap1b  |
| 2           | Overexpressed in normal bladder tissue | Human zinc finger transcription factor hEZF (EZF) homolog |
| 3           | Overexpressed in normal bladder tissue | Homo sapiens mRNA for phosphatidic acid phosphatase 2a    |
| 4           | Overexpressed in normal bladder tissue | H. sapiens mRNA for G protein-coupled receptor Edg-2      |
| 6           | Overexpressed in normal bladder tissue | Homo sapiens secreted frizzled-related protein            |
| 7           | Overexpressed in normal bladder tissue | Human monocytic leukemia zinc finger protein (MOZ)        |
| 4           | Overexpressed in normal bladder tissue | Homo sapiens angiotensin II receptor                      |
| 6           | Overexpressed in normal bladder tissue | Human mRNA for RNA helicase (HRH1)                        |
| 12          | Overexpressed in normal bladder tissue | H. sapiens rhoB   |
| 13          | Overexpressed in normal bladder tissue | Human skeletal muscle LIM-protein SLIM 1                  |
| 14          | Overexpressed in normal bladder tissue | Homo sapiens 39 kDa protein                               |
| 17          | Overexpressed in normal bladder tissue | H. sapiens dermatopontin mRNA                             |
| 18          | Overexpressed in normal bladder tissue | Homo sapiens phosphoglucomutase-related protein (PGMRP)   |

|    |  |   |
|----|--|---|
| 20 | Overexpressed<br>in normal<br>bladder tissue | Human nucleic acid binding protein<br>CNBP        |
| 21 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 22 | Overexpressed<br>in normal<br>bladder tissue | Human small nuclear<br>ribonucleoprotein (U1-70K) |
| 23 | Overexpressed<br>in normal<br>bladder tissue | H. sapiens mRNA for telokin homolog               |
| 24 | Overexpressed<br>in normal<br>bladder tissue | Homologous to pil2 from rats                      |
| 25 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 26 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 27 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 29 | Overexpressed<br>in normal<br>bladder tissue | Homologous to sushi repeat protein                |
| 30 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 31 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 32 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 33 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 34 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |

|    |  |   |
|----|--|---|
| 35 | Overexpressed<br>in normal<br>bladder tissue | Caenorhabditis elegans cosmid F09E5                                   |
| 36 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 37 | Overexpressed<br>in normal<br>bladder tissue | Homologous to murine RING zinc<br>finger protein                      |
| 38 | Overexpressed<br>in normal<br>bladder tissue | Rattus norvegicus cytoplasmic<br>dynein intermediate chain 2c         |
| 39 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 40 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 43 | Overexpressed<br>in normal<br>bladder tissue | Gry-rbp   |
| 44 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 46 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 47 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 48 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 50 | Overexpressed<br>in normal<br>bladder tissue | Homologous to HU-K5   |
| 51 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 52 | Overexpressed<br>in normal<br>bladder tissue | Homologous to O. aries putative G-<br>protein linked receptor (edg-2) |

|    |  |   |
|----|--|---|
| 53 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 54 | Overexpressed<br>in normal<br>bladder tissue | Human homolog to murine NST-1                                   |
| 55 | Overexpressed<br>in normal<br>bladder tissue | Homologous to human CIP4  |
| 56 | Overexpressed<br>in normal<br>bladder tissue | Human Chf5p homolog   |
| 57 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 58 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 59 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 60 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 61 | Overexpressed<br>in normal<br>bladder tissue | Caenorhabditis elegans cosmid TC9A5                             |
| 62 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 63 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 65 | Overexpressed<br>in normal<br>bladder tissue | Homologous to human KOX15                                       |
| 67 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 69 | Overexpressed<br>in normal<br>bladder tissue | Homologous to Golgi 4-transmembrane<br>spanning transporter MTP |

|    |  |   |
|----|--|---|
| 72 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 73 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 75 | Overexpressed<br>in normal<br>bladder tissue | Human homolog to rat mRNA for V-1<br>protein      |
| 77 | Overexpressed<br>in normal<br>bladder tissue | Caenorhabditis elegans cosmid F<br>13G3           |
| 78 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 79 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 80 | Overexpressed<br>in normal<br>bladder tissue | Human pyruvate dehydrogenase kinase<br>isoform 4  |
| 82 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 83 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 85 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 86 | Overexpressed<br>in normal<br>bladder tissue | Mouse epithelial zinc-finger<br>protein EZF (Zie) |
| 88 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 90 | Overexpressed<br>in normal<br>bladder tissue | Unknown   |
| 92 | Overexpressed<br>in normal<br>bladder tissue | Homologous to MyD118                              |



|     |  |  |
|-----|--|--|
| 93  | Overexpressed<br>in normal<br>bladder tissue | Homologous to p8 protein from rats                   |
| 94  | Overexpressed<br>in normal<br>bladder tissue | Unknown  |
| 95  | Overexpressed<br>in normal<br>bladder tissue | Unknown  |
| 96  | Overexpressed<br>in normal<br>bladder tissue | Homologous to murine B-1ND1                          |
| 97  | Overexpressed<br>in normal<br>bladder tissue | Canis familiaris Sec61-complex<br>gamma-subunit      |
| 98  | Overexpressed<br>in normal<br>bladder tissue | Unknown  |
| 99  | Overexpressed<br>in normal<br>bladder tissue | Human homolog to X taevis 146 kDa<br>nuclear protein |
| 100 | Overexpressed<br>in normal<br>bladder tissue | Unknown  |
| 101 | Overexpressed<br>in normal<br>bladder tissue | Human dysferlin                                      |
| 102 | Overexpressed<br>in normal<br>bladder tissue | Unknown  |
| 103 | Overexpressed<br>in normal<br>bladder tissue | Unknown  |
| 104 | Overexpressed<br>in normal<br>bladder tissue | Unknown  |
| 105 | Overexpressed<br>in normal<br>bladder tissue | Unknown  |
| 106 | Overexpressed<br>in normal<br>bladder tissue | Unknown  |

|     |  |   |
|-----|--|---|
| 107 | Overexpressed<br>in normal<br>bladder tissue | Unknown                                   |
| 108 | Overexpressed<br>in normal<br>bladder tissue | Homologous to APRIL                       |
| 109 | Overexpressed<br>in normal<br>bladder tissue | Homologous to the human p20               |
| 110 | Overexpressed<br>in normal<br>bladder tissue | Unknown                                   |
| 111 | Overexpressed<br>in normal<br>bladder tissue | Unknown                                   |
| 112 | Overexpressed<br>in normal<br>bladder tissue | Unknown                                   |
| 113 | Overexpressed<br>in normal<br>bladder tissue | Homologous to D. melanogaster<br>furrowed |
| 114 | Overexpressed<br>in normal<br>bladder tissue | Homologous to murine BRX protein          |
| 115 | Overexpressed<br>in normal<br>bladder tissue | Unknown                                   |
| 116 | Overexpressed<br>in normal<br>bladder tissue | Unknown                                   |
| 117 | Overexpressed<br>in normal<br>bladder tissue | Caenorhabditis elegans cosmid R08D7       |
| 118 | Overexpressed<br>in normal<br>bladder tissue | Unknown                                   |
| 119 | Overexpressed<br>in normal<br>bladder tissue | HSP 86                                    |
| 120 | Overexpressed<br>in normal<br>bladder tissue | Homologous to human AKAP95                |

|     |  |  |
|-----|--|--|
| 121 | Overexpressed in normal bladder tissue | Sus scrofa mRNA for 17-kDa PKC-potentiated inhibitory protein of PP1 |
| 122 | Overexpressed in normal bladder tissue | Unknown  |
| 123 | Overexpressed in normal bladder tissue | Homo sapiens supervillin   |
| 124 | Overexpressed in normal bladder tissue | Homologous to B. taurus vacuolar ATPase subunit A                    |
| 125 | Overexpressed in normal bladder tissue | SH3 domain binding glutamic acid-rich-like protein                   |
| 126 | Overexpressed in normal bladder tissue | Human homolog to Mus musculus WSB-1                                  |
| 127 | Overexpressed in normal bladder tissue | Unknown  |
| 391 | Lengthening to Seq. ID No: 27          |  |
| 392 | Lengthening to Seq. ID No: 34          |  |
| 393 | Lengthening to Seq. ID No: 50          |  |
| 394 | Lengthening to Seq. ID No: 56          |  |
| 395 | Lengthening to Seq. ID No: 78          |  |
| 396 | Lengthening to Seq. ID No: 82          |  |
| 397 | Lengthening to Seq. ID No: 88          |  |
| 398 | Lengthening to Seq. ID No: 100         |  |
| 399 | Lengthening to Seq. ID No: 101         |  |

|     |                                      |  |
|-----|--------------------------------------|--|
| 400 | Lengthening to<br>Seq. ID No:<br>102 |  |
| 401 | Lengthening to<br>Seq. ID No:<br>104 |  |
| 402 | Lengthening to<br>Seq. ID No:<br>110 |  |
| 403 | Lengthening to<br>Seq. ID No:<br>111 |  |

[Key to Table I:]

[Column 4: Sequence ID No. 109:] crystallin = crystalline

[Column 6: Sequence ID Nos. 6, 7, 9, 22, 29, 31-34, 39, 43, 46,  
48, 50, 51, 56, 58-62, 65, 72, 73, 82, 86, 102,  
103, 111, 112, 115, 126:] ... bis ... = ... to ...

TABELLE I

| Sequenz ID | Expression                           | Funktion  | Module                         | Cytogenetische Lokalisation | Nearest Marker            |
|------------|--------------------------------------|---|--------------------------------|-----------------------------|---------------------------|
| 1          | in Blasennormalgewebe überexprimiert | H sapiens rap1b   | ras                            | 6q21-q22.1                  | D6S304-D6S1639            |
| 2          | in Blasennormalgewebe überexprimiert | Human zinc finger transcription factor HEZF (EZF) Homolog | ZINC_FINGER_C2H2_2             |                             |                           |
| 3          | in Blasennormalgewebe überexprimiert | Homo sapiens mRNA for phosphatidic acid phosphatase 2a    |                                |                             |                           |
| 4          | in Blasennormalgewebe überexprimiert | H sapiens mRNA for G protein-coupled receptor Edg-2       | 7tm_1                          | 9q31.3-q32                  | D9S1690-D9S279            |
| 6          | in Blasennormalgewebe überexprimiert | Homo sapiens secreted frizzled-related protein            | FZ_DOMAIN; NETRIN_CT; PRO_RICH | 8p11.23-p12                 | SHGC-5722 bis SHGC-5765   |
| 7          | in Blasennormalgewebe überexprimiert | Human monocytic leukaemia zinc finger protein (MOZ)       |                                | 8p11.23-p12                 | D8S2070 bis SHGC-31558    |
| 8          | in Blasennormalgewebe überexprimiert | Homo Sapiens angiotensin II receptor                      |                                | 22q11.22-q11.23             | D6S2136-D4S3274           |
| 9          | in Blasennormalgewebe überexprimiert | Human mRNA for RNA helicase (HRH1)                        |                                | 6p21.31                     | SHGC-17229 bis D6S478     |
| 12         | in Blasennormalgewebe überexprimiert | H sapiens rhoB  |                                | 2p23.3                      | D2S387                    |
| 13         | in Blasennormalgewebe überexprimiert | Human skeletal muscle LIM-protein SLIM1                   | LIM_DOMAIN_2                   | Xq25-q27.2                  | DXS994-DXS1062            |
| 14         | in Blasennormalgewebe überexprimiert | Homo sapiens 39 kDa protein                               | PDZ; LIM                       | 4q34.1-q35.2                | D4S408-D4S426             |
| 17         | in Blasennormalgewebe überexprimiert | H sapiens dermatopontin mRNA                              |                                | 1q23.1-q23.2                | D1S445-D1S2750            |
| 18         | in Blasennormalgewebe überexprimiert | Homo sapiens phosphoglucomutase-related protein (PGMRP)   | PGM_PMM                        | 9p11.1-q12                  | D9S1699                   |
| 20         | in Blasennormalgewebe überexprimiert | Human nucleic acid binding protein CNBP                   | ZfCCHC                         | 3q13.31-q21.1               | D3S1589-D3S1766           |
| 21         | in Blasennormalgewebe überexprimiert | unbekannt   |                                |                             |                           |
| 22         | in Blasennormalgewebe überexprimiert | Human small nuclear ribonucleoprotein (U1-70K)            |                                | 19q13.31-q13.33             | SHGC-36947 bis SHGC-34723 |
| 23         | in Blasennormalgewebe überexprimiert | H sapiens mRNA for telokin Homolog                        |                                |                             |                           |
| 24         | in Blasennormalgewebe überexprimiert | Homolog zu p12 aus Ratte                                  |                                |                             |                           |

| Sequenz ID | Expression                           | Funktion   | Module            | Cytogenetische Lokalisation | Nearest Marker            |
|------------|--------------------------------------|--|-------------------|-----------------------------|---------------------------|
| 25         | in Blasennormalgewebe überexprimiert | unbekannt  |                   |                             |                           |
| 26         | in Blasennormalgewebe überexprimiert | unbekannt  |                   |                             |                           |
| 27         | in Blasennormalgewebe überexprimiert | unbekannt  |                   | 5q32-q33.1                  | D5S470                    |
| 29         | in Blasennormalgewebe überexprimiert | Homolog zu susII repeat protein                            | PRO_RICH          | 3q11.2                      | SHGC-36351 bis SHGC-14633 |
| 30         | in Blasennormalgewebe überexprimiert | unbekannt  |                   | 2q37.3                      | D2S206-D2S331             |
| 31         | in Blasennormalgewebe überexprimiert | unbekannt  |                   | 2q31.1-q31.3                | W1-7596 bis D2S326        |
| 32         | in Blasennormalgewebe überexprimiert | unbekannt  |                   | 20p13                       | D20S864 bis SHGC-34269    |
| 33         | in Blasennormalgewebe überexprimiert | unbekannt  |                   | 13q12.11-q12.3              | SHGC-2665 bis D13S289     |
| 34         | in Blasennormalgewebe überexprimiert | unbekannt  |                   | 9q21.31                     | SHGC-32247 bis SHGC-5528  |
| 35         | in Blasennormalgewebe überexprimiert | Caenorhabditis elegans cosmid F09E5                        | UPF0001           |                             |                           |
| 36         | in Blasennormalgewebe überexprimiert | unbekannt  |                   |                             |                           |
| 37         | in Blasennormalgewebe überexprimiert | Homolog zu murinem RING zinc finger protein                | PRO_RICH; ZF_RING | 17p13.3                     | D17S1548                  |
| 38         | in Blasennormalgewebe überexprimiert | Rattus norvegicus cytoplasmic dynein intermediate chain 2c | WD40_REGION       | 10q11.21                    | D10S804-D10S220           |
| 39         | in Blasennormalgewebe überexprimiert | unbekannt  |                   | 13q33.3                     | SHGC-9496 bis D13S1223    |
| 40         | in Blasennormalgewebe überexprimiert | unbekannt  |                   |                             |                           |
| 43         | in Blasennormalgewebe überexprimiert | Gry-rbp  | RBD               | 20p13                       | D20S816 bis SHGC-33687    |
| 44         | in Blasennormalgewebe überexprimiert | unbekannt  |                   |                             |                           |
| 46         | in Blasennormalgewebe überexprimiert | unbekannt  | f.                | 2q21.3-q22.1                | SHGC-35092 bis SHGC-32856 |
| 47         | in Blasennormalgewebe überexprimiert | unbekannt  |                   |                             |                           |

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| Sequenz ID | Expression                           | Funktion   | Module             | Cytogenetische Lokalisation | Nearest Marker            |
|------------|--------------------------------------|--|--------------------|-----------------------------|---------------------------|
| 48         | in Blasennormalgewebe überexprimiert | unbekannt  |                    | 15q11.2-q15.3               | SHGC-35142 bis SHGC-7407  |
| 50         | in Blasennormalgewebe überexprimiert | Homolog zu HU-K5   |                    | 3q21.3-3q23                 | SHGC-37132 bis SHGC-30693 |
| 51         | in Blasennormalgewebe überexprimiert | unbekannt  |                    | 3p21.31-p21.1               | SHGC-30574 bis SHGC-31529 |
| 52         | in Blasennormalgewebe überexprimiert | Homolog zu O. aries Putative G-protein linked receptor (edg-2) |                    |                             |                           |
| 53         | in Blasennormalgewebe überexprimiert | unbekannt  |                    |                             |                           |
| 54         | in Blasennormalgewebe überexprimiert | Humanes Homolog zu murinem NST-1                               | HSP70              |                             |                           |
| 55         | in Blasennormalgewebe überexprimiert | Homolog zu humanem CIP4  |                    |                             |                           |
| 56         | in Blasennormalgewebe überexprimiert | Humanes Cbl5p Homolog  |                    | Xq25-q27.3                  | SHGC-31168 bis AFM207xb8  |
| 57         | in Blasennormalgewebe überexprimiert | unbekannt  | ZF_DHHG; NLS_BP    |                             |                           |
| 58         | in Blasennormalgewebe überexprimiert | unbekannt  |                    | 9q12                        | WI-7387 bis SHGC-32868    |
| 59         | in Blasennormalgewebe überexprimiert | unbekannt  |                    | 9q22.2-q22.31               | SHGC-14680 bis SHGC-8725  |
| 60         | in Blasennormalgewebe überexprimiert | unbekannt  |                    | 1p36.13-p36.31              | SHGC-34104 bis SHGC-9861  |
| 61         | in Blasennormalgewebe überexprimiert | Caenorhabditis elegans cosmid T09A5                            |                    | Chr.5                       | SHGC-21758 bis SHGC-4278  |
| 62         | in Blasennormalgewebe überexprimiert | unbekannt  |                    | 1q32.3                      | SHGC-15949 bis SHGC-11476 |
| 63         | in Blasennormalgewebe überexprimiert | unbekannt  | Oxysterol_BP       | 1p32.3-p33                  | D1S197 D1S417             |
| 65         | in Blasennormalgewebe überexprimiert | Homolog zu humanem KOX15                                       | ZINC_FINGER_C2H2_2 | 16q21-q23.1                 | D16S2624 bis SHGC-9008    |
| 67         | in Blasennormalgewebe überexprimiert | unbekannt  |                    |                             |                           |
| 69         | in Blasennormalgewebe überexprimiert | Homolog zu Golgi 4-Transmembran spanning Transporter MTP       |                    | 8q22.3-q24.13               | D6S556 D6S266             |
| 72         | in Blasennormalgewebe überexprimiert | unbekannt  |                    | 10q23.1                     | SHGC-14535 bis SHGC-30780 |

| Sequenz ID | Expression                           | Funktion  | Module        | Cytogenetische Lokalisation | Nearest Marker            |
|------------|--------------------------------------|---|---------------|-----------------------------|---------------------------|
| 73         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               | 1q22                        | SHGC-32839 bis DIS1576    |
| 75         | in Blasennormalgewebe überexprimiert | Humanes Homolog zu Rat mRNA for V-ank 1 protein |               |                             |                           |
| 77         | in Blasennormalgewebe überexprimiert | Caenorhabditis elegans cosmid F13G3             | Ribosomal_L13 | 8q23.3-q24.11               | WI-5098-CHLC.GATA8G03.443 |
| 78         | in Blasennormalgewebe überexprimiert | unbekannt                                       | lg            |                             |                           |
| 79         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               |                             |                           |
| 80         | in Blasennormalgewebe überexprimiert | Humane Pyruvate Dehydrogenase Kinase Isoform 4  |               | 7q21.2-q22.1                | D7S482-D7S662             |
| 82         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               | 3p24.3-p23                  | SHGC-9648 bis SHGC-14769  |
| 83         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               | 3p12.1-p21.1                | D3S3117                   |
| 85         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               |                             |                           |
| 86         | in Blasennormalgewebe überexprimiert | Mouse epithelial zinc-finger protein EZF (Zie)  |               | 9q22.33-q31.1               | D9S1690 bis SHGC-14345    |
| 88         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               | 1p35.1                      | D1S2569-D1S2676           |
| 90         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               |                             |                           |
| 92         | in Blasennormalgewebe überexprimiert | Homolog zu MyD118                               |               |                             |                           |
| 93         | in Blasennormalgewebe überexprimiert | Homolog zum p8 Protein aus Ratte                | ras           | 16p11.2-q12.1               | D16S3093-D16S409          |
| 94         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               | 14q11.1-q11.2               | D14S990-D14S264           |
| 95         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               | 16p13.2-p13.3               | D16S521                   |
| 96         | in Blasennormalgewebe überexprimiert | Homolog zu murinem B-IND1                       |               | 15q22.31-q22.33             | D15S159-D15S125           |
| 97         | in Blasennormalgewebe überexprimiert | Canis familiaris Sec61-complex gamma-subunit    | SecE          |                             |                           |
| 98         | in Blasennormalgewebe überexprimiert | unbekannt                                       |               | 6p21.2-p21.31               | D6S276-D6S439             |



| Sequenz ID | Expression                           | Funktion  | Module                | Cytogenetische Lokalisation | Nearest Marker            |
|------------|--------------------------------------|---|-----------------------|-----------------------------|---------------------------|
| 99         | in Blasennormalgewebe überexprimiert | Humanes Homolog zu X laevis 146 kDa nuclear protein unbekannt |                       | 2q23.3-q33.3                | D2S117-D2S115             |
| 100        | in Blasennormalgewebe überexprimiert |   | NLS_BP                | 9q22.31-q31.1               | D9S176-D9S277             |
| 101        | in Blasennormalgewebe überexprimiert | Humanes Dysferlin   | PRO_RICH; C2_DOMAIN_2 |                             |                           |
| 102        | in Blasennormalgewebe überexprimiert | unbekannt   |                       | 10q25.3                     | D10S216 bis SHGC-13269    |
| 103        | in Blasennormalgewebe überexprimiert | unbekannt   |                       | 2p23.1-p23.2                | D2S2573 bis SHGC-16275    |
| 104        | in Blasennormalgewebe überexprimiert | unbekannt   | PRO_RICH              | 8p11.23-p12                 | D8S2102                   |
| 105        | in Blasennormalgewebe überexprimiert | unbekannt   |                       | 1p31.1-p34.1                | SHGC-32050                |
| 106        | in Blasennormalgewebe überexprimiert | unbekannt   |                       | 13q21.33-q22.1              | D13S156-D13S162           |
| 107        | in Blasennormalgewebe überexprimiert | unbekannt   |                       |                             |                           |
| 108        | in Blasennormalgewebe überexprimiert | Homolog zu APRIL  | TNF                   |                             |                           |
| 109        | in Blasennormalgewebe überexprimiert | Homolog zu dem humanem p20                                    | crystallin; HSP20     | 19q13.13                    | D19S425-D19S224           |
| 110        | in Blasennormalgewebe überexprimiert | unbekannt   |                       | 7q31.31                     | D7S522-D7S2756            |
| 111        | in Blasennormalgewebe überexprimiert | unbekannt   |                       | 10q23.31-q24.1              | WI-7908 bis SHGC-34547    |
| 112        | in Blasennormalgewebe überexprimiert | unbekannt   |                       | 1q31.1-q31.3                | SHGC-34113 bis SHGC-34344 |
| 113        | in Blasennormalgewebe überexprimiert | Homolog zu D. melanogaster furrowed                           | sushi                 | 9q31.3-q32                  | D9S160-D9S279             |
| 114        | in Blasennormalgewebe überexprimiert | Homolog zu murinem BRX Protein                                | PRO_RICH              |                             |                           |
| 115        | in Blasennormalgewebe überexprimiert | unbekannt   |                       | Chr. 17 (17p13.3-q25.3)     | SHGC-33067 bis SHGC-32338 |
| 116        | in Blasennormalgewebe überexprimiert | unbekannt   |                       | 4q28.1-q31.1                | D4S1580-D4S427            |
| 117        | in Blasennormalgewebe überexprimiert | Caenorhabditis elegans cosmid R08D7                           |                       |                             |                           |

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| Sequenz ID | Expression                           | Funktion   | Module                         | Cytogenetische Lokalisation | Nearest Marker         |
|------------|--------------------------------------|--|--------------------------------|-----------------------------|------------------------|
| 118        | in Blasennormalgewebe überexprimiert | unbekannt  | PRO_RICH                       |                             |                        |
| 119        | in Blasennormalgewebe überexprimiert | HSP 86   | HSP90                          | 11q13.2-q13.5               | D11S913-D11S1314       |
| 120        | in Blasennormalgewebe überexprimiert | Homolog zu humanem AKAP95  | PRO_RICH                       |                             |                        |
| 121        | in Blasennormalgewebe überexprimiert | Sus scrofa mRNA for 17-kDa PKC-potentiated inhibitory protein of PP1 | PRO_RICH                       | 19q13.13-q13.2              | D19S1069-D19S421       |
| 122        | in Blasennormalgewebe überexprimiert | unbekannt  |                                | 1q32.1                      | D1S306-D1S2570         |
| 123        | in Blasennormalgewebe überexprimiert | Homo sapiens Supervillin   | PRO_RICH                       |                             |                        |
| 124        | in Blasennormalgewebe überexprimiert | Homolog zu B laurus vacuolar ATPase subunit A                        |                                | 3q11.2-q21.1                | D3S2353-D3S3526        |
| 125        | in Blasennormalgewebe überexprimiert | SH3 domain binding glutamic acid-rich-like protein                   |                                | domain                      | binding                |
| 126        | in Blasennormalgewebe überexprimiert | Humanes Homolog zu Mus musculus WSB-1                                | WD40_REGION; WD40; SOCS_DOMAIN | 17p11.2                     | D17S783 bis SHGC-30289 |
| 127        | in Blasennormalgewebe überexprimiert | unbekannt  |                                |                             |                        |
| 391        | Verlängerung zu Seq ID No: 27        |  |                                |                             |                        |
| 392        | Verlängerung zu Seq ID No: 34        |  |                                |                             |                        |
| 393        | Verlängerung zu Seq ID No: 50        |  |                                |                             |                        |
| 394        | Verlängerung zu Seq ID No: 56        |  |                                |                             |                        |
| 395        | Verlängerung zu Seq ID No: 78        |  |                                |                             |                        |
| 396        | Verlängerung zu Seq ID No: 82        |  |                                |                             |                        |
| 397        | Verlängerung zu Seq ID No: 88        |  |                                |                             |                        |
| 398        | Verlängerung zu Seq ID No: 100       |  |                                |                             |                        |
| 399        | Verlängerung zu Seq ID No: 101       |  |                                |                             |                        |

| Sequenz ID | Expression                     | Funktion | Module | Cytogenetische Lokalisation | Nearest Marker |
|------------|--------------------------------|----------|--------|-----------------------------|----------------|
| 400        | Verlängerung zu Seq ID No. 102 |          |        |                             |                |
| 401        | Verlängerung zu Seq ID No. 104 |          |        |                             |                |
| 402        | Verlängerung zu Seq ID No. 110 |          |        |                             |                |
| 403        | Verlängerung zu Seq ID No. 111 |          |        |                             |                |

TABLE II

Seq. ID No.                      Peptide Sequences (ORF's)                      Seq. ID. No.

| Seq. ID. No. | Peptid-Sequenzen (ORF's) | Seq. ID. No. |
|--------------|--------------------------|--------------|
| 21           |                          | 430          |
|              |                          | 431          |
| 24           |                          | 128          |
|              |                          | 129          |
| 25           |                          | 131          |
|              |                          | 132          |
|              |                          | 133          |
| 26           |                          | 134          |
|              |                          | 135          |
|              |                          | 136          |
| 27           |                          | 137          |
|              |                          | 138          |
|              |                          | 139          |
| 29           |                          | 143          |
| 30           |                          | 144          |
|              |                          | 145          |
|              |                          | 146          |
|              |                          | 147          |
|              |                          | 148          |
| 31           |                          | 149          |
|              |                          | 150          |
|              |                          | 151          |
|              |                          | 152          |
| 32           |                          | 153          |
|              |                          | 154          |
|              |                          | 155          |
| 33           |                          | 156          |
|              |                          | 157          |
| 34           |                          | 158          |
|              |                          | 159          |
|              |                          | 160          |
| 35           |                          | 161          |
|              |                          | 162          |
|              |                          | 163          |
| 36           |                          | 164          |
|              |                          | 165          |
|              |                          | 166          |
| 37           |                          | 167          |
| 38           |                          | 168          |
| 39           |                          | 169          |
|              |                          | 170          |
|              |                          | 171          |
| 40           |                          | 172          |
|              |                          | 173          |
|              |                          | 174          |
| 43           |                          | 181          |
| 44           |                          | 182          |
|              |                          | 183          |
|              |                          | 184          |

Seq. ID No.

Peptide Sequences (ORF's) Seq. ID. No.

| Seq. ID. No. | Peptid-Sequenzen (ORF's) | Seq. ID. No. |
|--------------|--------------------------|--------------|
| 46           |                          | 188          |
|              |                          | 189          |
|              |                          | 190          |
| 47           |                          | 191          |
|              |                          | 192          |
|              |                          | 193          |
| 48           |                          | 194          |
|              |                          | 195          |
|              |                          | 196          |
| 50           |                          | 200          |
|              |                          | 201          |
|              |                          | 202          |
| 51           |                          | 203          |
|              |                          | 204          |
|              |                          | 205          |
| 52           |                          | 206          |
|              |                          | 207          |
|              |                          | 208          |
| 53           |                          | 209          |
| 54           |                          | 210          |
| 55           |                          | 211          |
| 56           |                          | 212          |
|              |                          | 213          |
|              |                          | 214          |
| 57           |                          | 215          |
| 58           |                          | 216          |
|              |                          | 217          |
|              |                          | 218          |
| 59           |                          | 219          |
| 60           |                          | 220          |
|              |                          | 221          |
|              |                          | 222          |
|              |                          | 223          |
| 61           |                          | 224          |
|              |                          | 225          |
| 62           |                          | 226          |
|              |                          | 227          |
|              |                          | 228          |
| 63           |                          | 229          |
| 65           |                          | 233          |
| 67           |                          | 237          |
|              |                          | 238          |
|              |                          | 239          |
| 69           |                          | 243          |
|              |                          | 244          |
| 72           |                          | 251          |
|              |                          | 252          |
|              |                          | 253          |
| 73           |                          | 254          |
|              |                          | 255          |
|              |                          | 256          |
| 75           |                          | 260          |
| 77           |                          | 264          |

Seq. ID No.

Peptide Sequences (ORF's) Seq. ID. No.

| Seq. ID. No. | Peptid-Sequenzen (ORF's) | Seq. ID. No. |
|--------------|--------------------------|--------------|
| 78           |                          | 265          |
|              |                          | 266          |
|              |                          | 267          |
| 79           |                          | 268          |
|              |                          | 269          |
| 80           |                          | 270          |
|              |                          | 274          |
|              |                          | 275          |
| 82           |                          | 276          |
|              |                          | 277          |
|              |                          | 278          |
| 83           |                          | 279          |
|              |                          | 283          |
|              |                          | 284          |
| 85           |                          | 285          |
|              |                          | 286          |
|              |                          | 287          |
| 86           |                          | 288          |
|              |                          | 292          |
|              |                          | 293          |
| 88           |                          | 294          |
|              |                          | 298          |
|              |                          | 299          |
| 90           |                          | 300          |
|              |                          | 304          |
|              |                          | 305          |
| 92           |                          | 306          |
|              |                          | 307          |
| 93           |                          | 308          |
|              |                          | 309          |
|              |                          | 310          |
| 94           |                          | 311          |
|              |                          | 312          |
|              |                          | 313          |
| 96           |                          | 314          |
|              |                          | 315          |
|              |                          | 316          |
| 98           |                          | 317          |
|              |                          | 318          |
|              |                          | 319          |
| 99           |                          | 320          |
|              |                          | 321          |
| 100          |                          | 322          |
|              |                          | 323          |
| 101          |                          | 324          |
|              |                          | 325          |
|              |                          | 326          |
| 102          |                          | 327          |
|              |                          | 328          |
|              |                          | 329          |
| 103          |                          | 330          |
|              |                          | 331          |
|              |                          | 332          |
| 104          |                          | 333          |
|              |                          |              |
| 105          |                          |              |
|              |                          |              |

## |Peptid-Sequenzen (ORF's) Seq. ID. No.

397

Seq. ID No.

Peptide Sequences (ORF's) Seq. ID. No.

| Seq. ID. No. | Peptid-Sequenzen (ORF's) | Seq. ID. No. |
|--------------|--------------------------|--------------|
| 126          |                          | 388          |
| 127          |                          | 389          |
|              |                          | 390          |
| 391          |                          | 404          |
|              |                          | 405          |
| 392          |                          | 406          |
|              |                          | 407          |
| 393          |                          | 408          |
|              |                          | 409          |
| 394          |                          | 410          |
|              |                          | 411          |
| 395          |                          | 412          |
|              |                          | 413          |
| 396          |                          | 414          |
|              |                          | 415          |
| 397          |                          | 416          |
|              |                          | 417          |
| 398          |                          | 418          |
|              |                          | 419          |
| 399          |                          | 420          |
|              |                          | 421          |
| 400          |                          | 422          |
|              |                          | 423          |
| 401          |                          | 424          |
|              |                          | 425          |
| 402          |                          | 426          |
|              |                          | 427          |
| 403          |                          | 428          |
|              |                          | 429          |

The inventive nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 128-390 and 404-431 are described in the following sequence protocol.



**Sequence Protocol****(1) GENERAL INFORMATION:****(i) APPLICANT:**

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

**(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Normal Bladder Tissue****(iii) Number of sequences: 365****(iv) COMPUTER-READABLE FORM:**

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

**(2) INFORMATION ON SEQ ID NO. 1:****(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1722 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

**(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing****(iii) HYPOTHETICAL: NO****(iii) ANTI-SENSE: NO****(vi) ORIGIN:**

- (A) ORGANISM: HUMAN
- (C) ORGAN:

**(vii) OTHER ORIGIN:**

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

cgttgaagta gatgcacaac agtgtatgct tgaatcttgc gatactgcag gaacggagca 60
atttacagca atgagggatt tatacatgaa aaatggacaa ggatttgcatt tagtttattc 120
catcacagca cagtccacat ttaacgattt acaagacctg agagaacaga ttcttcgagt 180

taaaacacct gatgatgttc caatgattct tgttggtaat aagtgtgact tgggaagatga 240
aagagtgtga ggggaaggaac aaggtcaaaa tctagcaaga caatgggaaca actgtgcaat 300
cttagaattc tctgcacaaat caaaaataaaa tgttaatgag atctttttatg acctagtgcg 360
gcaaatatac agaaaaaaccc cagtgcctgg gaaggctcgc aaaaagtcac catgtcagct 420
gcttttaatar actaaatgca ttgtagctct gagccaggtc tgaagaactg ttgcccaatt 480
caacagtgcc agcattccaa ctttgtttaa cctaccaaca tctttaaattg accttccctgt 540
ggtgggtaccc ttttaagaggc ggaatgaaagc tactatatca gtttgcacat tctaatcact 600
ttccagtatc acaagagaga tttttactta tataatagtc cttagagtttg cagctgggtaa 660
aacCagaggc tacatccagt attactgcta agagacattc ttcatccacc aatgttgtag 720
atgtatgaaa atggtgtact gtataccttta acatgcccca tactttgtat tggagagtag 780
aataatgtaa atcctaaaaag caccactatt ttagcataat aaaaagaagt ccaaaagagct 840
cctatataga ctactccaga taacttcgct tctttgatac ttgtagctta ttgtaatatt 900
ttttaagaaa tccaagggtca ttattattgt acaaaaataag cgctttgatt aacacagcta 960
tatagttttt ttaattttta aaaaacctgt ggagacgggt atcttgcctt taaaacatga1020
tagtcccttc agtataatgt cttagattaa agacgttgcc ttttaatatc gttgggaagg1080
aaatgtccag acttttccaa tctcttatta tatgtttcct ttttttggtt acataggggaal140
caatgtttat agtctgtgtg acagtggggg totacaacaa gaagtgtata ttttcaaaal200
atttttttaat gatttaacaa tttttgtaaa tcattttcag gcttctgcag ctgtagattc1260
tcactgtgaa tcccttgctc gctcatgcac aagtgtattt gcaatacca atatacaggt1320
ttagtatttt tgcctgttag tgattgtttc acatgtgtaa cgttttgggt gagatgttaa1380
atggtgtgag agtactgttg atgtgaatgt gggaagtaat ttttaacata tgtaattgtt1440
cacaaggcct aatttgcagt aactattgct gttttattta acaatgcctt gttgctttgt1500
atgcattaat gtttggagct aaagattgtg tgtctatcca acaggggacc acagtattta1560
aattgaccaa cctaatgtca caactacttt gaggtggcca tgttaaact aaaagtctta1620
atttaaagtgg tgcaattttg tataacttag catcagtagt tcaataaatt tggatttgcca1680
tgcaagggct tgcattataa aaaaaaacaa aaaaaaaaaa aa 1722

```

## (2) INFORMATION ON SEQ ID NO. 2:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1187 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

cggtctgagg agggcggttt ttgtgcacc caactggggg ctggaccccc tctcagcaat 60
ggccaccggc cggtctgcaca cgaactcccc ctgggggggg actccccagc aggactaccc 120
cgaccctggg tcttgaggaa gtgttgagca gcaggggactg tcaccctgcc ctgcccgcttc 180
ctcccggttt ccattccccac ccggggccca attaccatc cttcctgccc gatcagatgc 240
agccgcgaagt cccgcgcgtc cattaccaag agctcatgcc acccggttcc tgcattgccag 300
aggagcccaa gccaaagagg ggaagacgat cgtggccccc gaaaaggacc gccaccacca 360
cttgtgatta cgcgggctgc ggcaaaacct acacaaagag ttcccatctc aaggcacacc 420

tgcgaaccca cacaggtgag aaaccttacc actgtgactg ggacggctgt ggatggaaat 480
tcgcccgcctc agatgaactg accaggcact accgtaaaac cacggggcac cgcccgttcc 540
agtgcacaaa atgcgaccca gcattttcca ggtcggacca cctcgcccta cacatgaaga 600
ggcattttta aatccccagc agtggatag accacactg ccagaagaga attcagatatt 660
ttttactttt cacactgtct tcccgatgag ggaaggagcc cagccagaaa gcactacaat 720
catggtcagg ttcccactgc agtcatcttg tgagtggata atcaggaaaa atgaggaaac 780
caaaagacaa aaatcaaaag acagatgggg tctgtgactg gatcttctat cattccaatt 840
ctaaatccga cttgaatatt cctggactta caaaatgcca agggggtgac tggaaagttgt 900
ggatatcagg gtataaatta tatccgtgag ttgggggagg gaagaccaga attcccttga 960
attgtgtatt gatgcaatat aagcataaaa gatcaccttg tattctcttt accttctaaa1020
agccattatt atgatgttag aagaagagga agaaattcag gtacagaaaa ccatgtttaa1080
atagcctaatt gatggtgttt gtgagcttgg tcctaaaggt cccaacaagg gagccaaaagg1140
tttaaacctc tggatccctg gcaaggggaa atctgtgttt ttttccg 1187

```

## (2) INFORMATION ON SEQ ID NO. 3:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1478 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

gcgaacccgc gcgctgcccc gtccctgcgct gccacagcgg aggggctgga ccccgcggtc 60
ctccctccctg ccgggtcccca tccttaaaag gagagtctgg acgccccgcc tgtggggagag 120
agcgccggga tccggacggg gagcaaccgg gccagggccgt gccggctgag gaggtctctga 180
ggctacagag ctgcggccggc tggcacacga gcgcctcgcc actaacccag tgttccgggg 240
ggctgtgagg ggagggccccc gggcgccatt gctggcggtg ggagcgccgc ccggtctccag 300
cccgccctcg gctgctctcc tcctccggct gggagggggc gtgctcggg gccgtcgcca 360
gccccggccc gggtctcgaga atcaagggcc tcggcccgcc tcccgcgct cagtccatcg 420
cccttgcggg gcagcccggg gagagaccat gtttgacaag acgcgcgctgc cgtacgtggc 480
cctcgatgtg ctctgcgtgt tgcctggctgg attgcctttt gcaattctta ttcaaggca 540
taccoccttc caacgaggag tattctgtaa tgatgagtcc atcaagtacc cttacaaga 600
agacaccata ccttatgcgt tattaggtgg aataatcatt ccattcahta ttatcgttat 660
tattcttggg gaaacccctg ctggttactg taaccttttg cactcaaat cctttatcag 720
gaataactac atagccacta ttacaaaag cattggaacc tttttatttg gtgcagctgc 780
tagtcagtc ctagctgaca ttgccaahta ttcaataggc agactgcggc ctcaactctt 840
ggatgtttgt gatccagatt ggtcaaaaat caactgcagc gatggttaca ttgaatacta 900
catatgtcga gggaatgcag aaagagttaa ggaaggcagg ttgtccttct attcaggcca 960
ctcttcgttt tccatgtact gcattgctgt tgtggcactt tatcttcaag ccaggatgaal1020
gggagactgg gcaagactct tacgcccac actgcaattt ggtcttgttg ccgtatccat1080

actctgtggc cttctcgag tttctgatta taaacaccac tggagcgatg tgttgactgg1140
actcattcgg ggagctctgg ttgcaatatt agttgctgta tatgtatcgg attttcttcaal1200
agaaaagaact tcttttaaaag aaagaaaaga ggaggactct catacaactc tgcattgaac1260
accaacaact gggaatcact atccgagcaa tcaccagcct tgaaggcgag cagggtgccc1320
aggtgaagct ggctgttttt ctaaaaggaaa atgatttgcca caaggcaaga gggatgcatc1380
tttcttcccg ggtgtacaag cctttttaa gaccttctgc tggctgcgat gcctcttggga1440
atgcacagtt gtgtgtaaca gagttacctt aactcgtg 1478

```

## (2) INFORMATION ON SEQ ID NO. 4:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 411 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

gccacatttc cgggggttttg cgggccccgc gatgttttcc agagcttttc aagtgggaag 60
aggagagcga caacgtgaaa atgccccgtg cgggggcgtc caccggagtc ctgccagctg120
tccggcgctg ggggtggacgt ctgatttatg aagctcccca tccacctatc tgagtacctg180
acttctcagc actgacacct acagcatcag gtacacagct tctcctagca tgacttcgat240
ctgatcagca aacaagaaaa tttgtctccc gtagtctcgg ggctgtgtca ccacctacaa300
ccacagagct gtcatggctg ccatctctac ttccatccct gtaattttcac agccccagtt360
cacagccatg aatgaaccac agtgcttcta caacgagtcc attgccttct t 411

```

## (2) INFORMATION ON SEQ ID NO. 6:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3181 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

cggtgggggt  gggagcaggg  ggggacagtg  ccccgggaac  cgggtgggtc  acacacacgc  60
actgcgctgt  ttagtagtgg  acattgtaat  ccagtcggct  tgttcttgca  gcattccgcg  120
tcccttccct  ccatagccac  gctccaaacc  ccaggttagc  catggccggg  taagacaaag  180
gccatttaga  ttaggaaagt  ttttaagatc  cgcaatgtgg  agcagcagcc  actgcacagg  240
aggaggtgac  aaaccatttc  caacagcaac  acagccacta  aaacacaaaa  agggggattgt  300
ggcggaagt  gagagccagc  agcaaaaaac  acattttgca  actgttggt  gttgattctat  360
tggctgatct  atgcttttca  actagaaaaa  totaatgatt  ggcaagtcaac  gttgtrttca  420
gttccagagt  agrttttttc  tgtctgcttt  aaatggaaac  agactcatat  cacactttaca  480
attaaggtca  agcccagaaa  gtgataagtg  cagggaaggaa  aagtgcgaag  cacttatgtca  540
atagtgcagc  caaaggggac  agggggagag  cattgccttc  tctgccacaa  gtct  600
gtgattgttc  ttgaattctg  atcagccagt  ctcagatgcc  ccaaagtctc  ggtttcctatg  660
agccccgggc  atgatctgat  ccccagacac  tgtggagggg  cagcctgtgc  ctgcctttgt  720
gtcagaaaaa  ggaacccaca  gtgagcctga  gagagacgct  gattttcggg  ctgagaaggc  780
agtagttttc  aaaaacacata  gttaaaaaag  aaacaaatga  aaaaaatttt  agaacagcttc  840
agcaaatxgc  tagtcaagggt  gaattgtgaa  attgggtgaa  gagcttagga  ttctaattct  900
atgttttttc  cttttccacat  ttttaaaaag  acaatgacaa  acacccactt  atttttccag  960
gttttaaaac  agtctacatt  gagcatttga  aaggcgtgct  agaacaagggt  cctctgatcc  1020
gtccgagggt  ggtctccaga  ggagcagctc  tcccaggaca  ttgcccagg  gagggcgat  1080
tcccttgtag  ttgagtgtgt  tggctttctc  tctgtgaagag  tccgttggtt  cctgagaacc  1140
taacaccccc  tagcaaaact  cacagagctt  tccgtttttt  tctttcctgt  aaagaacact  1200
ttcctttgaa  ctgtattgct  tatggatcaa  agaaaattcag  aacagccctg  ctgtccccc  1260
gcaatttttc  catatatttg  ttctatttct  gcagatggaa  agttgacatg  ggtggggtgt  1320
ccccatccag  cgagagagtt  tcaaaaagcaa  aacatctctg  cagttttttc  caagtacct  1380
gagatacttc  caaagccct  tatgtttaat  cagcgatgta  tataagccag  ttcacttaga  1440
caacttttac  cttcttgtcc  aatgtacagg  aagtgttct  aaaaaaaatg  catatttaatt  1500
tcttccccc  aagccggatt  cttaattctc  tgcacacatt  tgaggacatt  tatgattgtc  1560
cctctgggct  aatgctttata  cccagtgagg  atgctgcagt  gaggtctgtaa  atgtggcccc  1620
tgccggccct  gccagaccgc  gaggaaggga  tggtagattc  tgttaactct  tgaagactcc  1680
agtatgaaaa  tcagcatgcc  cgcctagtta  cctaccggag  agttatcctc  ataaaattaac  1740
ctctcacagt  tagtgatctc  gtctttttaa  cacttttttt  gtggggttct  ctctgacctt  1800
tcatctgtaa  gtctgggga  ccttaagtga  ttgtcctgt  atttttgatg  attaaaaaat  1860
gtgtatata  attagctaat  tagaaaatatt  ctacttctct  gttgtcaaac  tgaiaattcag  1920
agcaagttcc  tgaagtgcgt  gatctgggtc  ttagttctgt  ttgattcaat  caagagttcal  1980
gtgctcatac  gtatctgctc  attttgacaa  agtgccctac  gcaaccgggc  cctctctctg  2040
cgccagagtc  cttagtgagg  ggggttaact  ggaacattag  tagttaccac  agaatacagg  2100
agagcagggt  actgtgctgt  gcagctctct  aaatgggaat  tctcaggtag  aagacaaacag  2160
cttcagaaa  agctcaaaaat  aaattggaaa  tgtgaatcgc  agctgtgggt  ttaccaccgg  2220
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catagcagct  ttgtctctgt  cacatcagca  atttcagaac  caaaaggagg  gctctctgta  2340
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tggccgttct  gacctgttgc  cagcagatgc  acaggacatg  gatgaaatct  cgttttctct  2940
tagtttcttc  ctgtagtact  cctcttttag  atcctaagtc  tcttcaaaaa  gctttgaata  3000

```

```

ctgtgaaaat  gttttacatt  ccatttcatt  tgtgttgttt  ttttaactgc  attttaccag  3060
atgtttttgt  gttatogett  atgttaatag  taattccocgt  acgtgttcat  tttattttca  3120
tgctttttca  gccattgtac  aatattcaact  tgactaaaaat  caactcaatta  atcaataaaa  3180

```

## (2) INFORMATION ON SEQ ID NO. 7:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1964 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

gcâacatgtc  tggccaccaac  attggcattc  ctccacacgca  gagattgcaa  gggcaaatgc  60
cagtgaaggg  gcacattttcc  atccgctcca  agtctcgcgcc  actgccctct  cggcgctgctc  120
accagcagca  gctgtatggc  cgtagcccat  cggcagtgctc  catgcaggtc  ggccctcgcg  180
cactggctgt  tcagcgtggc  atgaacatgg  gggtttaact  gatgcctact  cccgcctata  240
atgtcaattc  catgaatatg  aacaccttga  atgccatgaa  cagctatcga  atgacacagc  300
ccatgatgaa  cagcagttac  catagtaacc  ctgcctacat  gaaccagaca  gcacagttac  360
ctatgcagat  gcagatggga  atgatgggga  gccaggccta  tacccagcag  cctatgcagc  420
ctaaccctca  tggggaacatg  atgtacacag  gccctcccca  tcacagctac  atgaacgctg  480
ctggcgctgc  caagcagtca  ctcaacggac  cttacatgag  aagatgagca  agatgaactt  540
gcaatcaaaa  acttaaatat  atataaataa  aggaaccttt  tatactgaca  aaccagagaa  600
aaatggacct  ttttccagtt  aaaatatgtc  tgtagattta  gaggaatttt  tctttgggtt  660
attttatttt  ttgaaaaacc  tgatcttttc  tttttttggg  ttcatattgt  tctgggtttt  720
ggttttcttc  acaatcttga  acatttttaca  gtagaactca  tctaaaaatg  gatttgggga  780
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agaccccttc  ctccaaaccc  aacctttcat  ttctacttct  attccagcag  gaggcactta  1020
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caaatccagc  ctttgaggga  atagagatgg  tcaattaaca  atcaaaaaag  ggagattaac  1380
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gataaaaact  aaatagcagt  ccccgatgat  ttgcctctta  ggttctttct  taaattgttg  1560
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gtagctattt  aagtgtatca  tacctctagt  ttttgtatgt  cttttgagat  cctgagttca  1740
tccctgtgta  atcagatgtc  acaagcacct  ctccgtgtgag  tggctaata  gaagagggac  1800
agaccgacca  ccagcacagt  aggcagatc  tggacagcag  aatgttata  cgaagttca  1860
tgtgttgctc  ccaactccat  tctcttttct  ctctgtcaac  cagtttgccc  attctcttcc  1920
tattacttgc  tcCagggata  ggtaaaaaaa  aaaaaaaaaa  aaaa  1964

```



## (2) INFORMATION ON SEQ ID NO. 8:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1702 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

ggacacccca ggtatgtgga cgagcagttc ctgtcaccgc tttctctatt tgtggccctg 60
gtgatcatgt tctggctcct gattgcctaa tgctgggctc ctgcgtacat ccgtggcagg 120
gctctggact ggtgacgtgc caccocaaact cctgggtgtt ggcttccctg ctaactctga 180
ctcctggaat cagtggggtc agtaacacat caaggagtct tgtttcttca tcagagcttt 240
ggaactcgag accagttggc gatgacccct gaatatgcc accgctgtaa acactctata 300
acttcaggcc ttggcattga gtcactcttc atgggtgaca ccatgaaatc ttgtttcagc 360
cagttctgca ggtcctgact ctgcagaggg aagaggcaga aagagagaaa ctgtcagagt 420
ataatttcac ctgagtttaa tattacagaa acaaaaggat gcaccaaagt gtaattcttg 480
aaattttcat gtctttaaat accccttggt aagttgcttc tgaagccagt gggggctcct 540
cagatagaga ggttcccccct tcaaatccca gtgccgtctt gttctcttcc ctccccctcc 600
cactcccccct ctctctctcc tgtagagatg caagaaattg ctgtcccata aaaatcataa 660
ttgcagtagc taaagctggg gtcacttctg gaattccaca gagactcaaa gatcttttat 720
tggctctggg ctgtgctcag tgtctttggc ctccagagaa aacttgaagt acctctgggt 780
ttctctggcat aaattattcc tgggtgagaca tgtggcttaa ctccacaggt tcccatcagc 840
ttctctccca aaactatgtt catctgcctc tctctgccag agaacataca gccgagaata 900
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tcttccctcc tgtggaatgg aggggaaatt attctccca ataccttgtat ttgattttcal 1380
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tcttctctga gaccccaaaag ctggaggagg atgggcttct ctctgggccc ctcttctctac 1560

tttgcacatc acactgtctc tggcctaacc cagcaagaac caacaaatgg gttagggaagc 1620
cccatcaaat tggctttttt tcttcaatta tggacgtgca ttgttttggt tgggaacaaal 1680
aggtttttga ggggagatgt gg

```

1702

## (2) INFORMATION ON SEQ ID NO. 9:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2067 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

gcccagagct ccgcgtgttc ccatttcgag aggagctcct ggctgctatt gcaaatcacc 60
aagtctctcat cattgaaggg gagacagggt cagggaagac caccagatgc ccgcagtatc 120
tcctttgagga gggttataca aacaagggtat tgaagattgc ctgcacccaa ccccgagagc 180
tggtcccatc gagtgtggcc gcccgagtg ccggggagat ggggtgtgaag cttgggaatg 240
aggttggcta cagcatccgc tttaggaact gcacatcaga gcgaactgtc ctccgtatca 300
tgacagatgg gatgtcttc cgggagtctc tctctgagcc tgacctggcg agttacagcg 360
tggtgatggt ggaatgagca cacgaaggga cctacacac agacattctc ttggattga 420
tcaagatgtg tgcctcgttc cgacctgagc tcaaggctct ggtggcttca gccacaatgg 480
acactgccc tttttccacc ttctttgatg acgcccctgt gtttcgaatc cccggacgca 540
ggtttctctg ggacatcttc tacaccaagg ctccagaggg tgactacttg gaagctttgtg 600
tagtatctgt gttgcagatc catgtgacct agccccctgg ggatatcctg gtgttctctga 660
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aggcccgat ctccacgccc acaccacctg gggcacgaaa ggtggtttgtg gcaaacgaaca 840
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aggcctcagc caatcagcga gctggcaggg caggtcgggg ggctgcaggg aagtgtctcc 1020
gctctatcac cgcttgggcc tatcagcacg agcttgagga aaccacagct cctgagatcc 1080
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gaccaaagga caaggctgctc catgctgaca atgcccgtgt caacttcttt ctccctggcg 1440
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ataaagccaa ggaagctctga gatccccatg tcaagaaaaa gccagcaaaa ataggcaaaa 1920
cacgagaaga gctaggggtaa gagaaggacg taaacagaac ctgacaccaa ctctttttcc 1980
ttctatcatc tatttaaatc ctattaaata aaattatttt tggaataaag cttgtgggaa 2040
cattttggat ctagaaaaaa aaaaaaa

```

2067

## (2) INFORMATION ON SEQ ID NO. 12:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

gcccgcagccc  tcatctgccca  cccgagctctg  gttggagctg  ttgtcttcta  tgctcagoga  60
ggcccgaggaga  gaccocgggag  agagctaggc  agagtccacc  gcccgagctct  gctgcccgag  120
cccgcgttac  gcacaaaacc  gccgatcccc  ggcctggggg  gagcagagcg  accaccggcc  180
gggagcagcg  cggcgagacg  cccggtgcgc  cctatgcccc  cgcgccccca  ccgcccccg  240
cgcgccagcc  gaagcgcagc  gagagaacgc  gccaccgcgg  ggcccggggt  cagctagoga  300
ccctctcgcc  acctgcgcgc  agcccgaggt  gagcagtgag  cggcgagcgg  gagggcagcg  360
aggcggttcg  gggcccccct  ctgctgcgcc  ggcccgggcc  tcattggcgc  catccgcaag  420
aagctgggtg  tggctggcgga  cggcgcggtg  ggcaagacgt  gcctgctgat  cgtgttcagt  480
aaggacaggt  tccccgaggt  gtacgtgccc  accgtctctg  agaactatgt  ggccgacatt  540
gaggtggagc  gcaagcaggt  ggaggtggcg  ctgtgggaca  cggcgggcca  ggaggactac  600
gaccgcgtgc  ggccgctctc  ctaccgggac  accgagctca  ttctcatctg  cttctcgtgt  660
gacagcccg  actcgtctga  gaacatcccc  gagaaagtg  tccccgaggt  gaagcacttc  720
tgtcccaatg  tgcccatcat  cctggtggcc  aacaaaaaag  acctgcgcag  gacgagcatg  780
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tgccgagag  ctctogagac  gccacgcgc  ccgcgctgca  gaagcgctac  ggctccca  960
accggtgc  caactgcgc  aaggtgctat  gagggccgc  cccgtcgcgc  ctgccctgc  1020
cggcgaggt  tccccctctg  gaccagtccc  ccgcgagccc  ggagaagggg  agaccctgt  1080
cccacaaaga  ccccaccgc  ctgcctggca  tctgtctgt  gacgcctctg  tctggccca  1140
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cacaggccgc  ggctccccac  tgagtgcaca  ggggtccctg  agcatgcttt  tctgaagaga  1260
cggcgctcag  agtgtgtggc  tgtgtgtct  ttgactccc  ctgcgcccat  ttaccaccca  1320
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tgccggaggg  ggggctgct  ggggaggtg  gggggtgtt  atataaat  agataaat  1500
tcatcttcg  agctaagatg  gtgttattta  aggtgtgta  tgggtgagcg  ctctggccca  1560

```

```

ggctggggcca gactcccgcc caagcatgaa caggacttga ccatctttcc aaccctggg1620
gaagacattt gcaactgact tggggaggac acagcttcag cacagcctct cctgcggggcc1680
agcccgctgc gaacccctcca ccagctaccg gagggaggag ggaggatgcg ctgtgggggtt1740
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ttgtgatttt attttgtcag gtcatgcaca cagttttgat aaagggcagt aacaagtatt2100
ggggcctatt tttttttttt tccacaaggc attctctaaa gctatgtgaa attttctctg2160
cacctctgta cagagaatac acctgcccct gtatatcctt ttttccccc cctccctcc2220
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tatgtaaaat attaaaagac tatgatgatg acatttttat aaagaaatc ttgtgggtta2400
atagtctgta aaaatccct tgtgaatttg gaacaaggga gatattctcc taggcgagat2460
cctttcttgc caactccgtt tcccttatag caaatgtagt aaatgaggat gaagtccctt2520
tgagagcatg tggggggttg gtgaccaa

```

2548

(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1673 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

|            |             |             |             |             |             |      |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| accaatgac  | atgtagtaat  | caaatgtttg  | gggctagata  | ttatggtata  | caaaaaacat  | 60   |
| taaaatcatg | tggtttgcaa  | gcaaaagcaaa | catttttgcc  | aatgtttgca  | aattggccac  | 120  |
| aaccacaaat | tcaagaaatt  | ttttaaaaag  | acaaaagcca  | gcttacaaga  | atttgaccaa  | 180  |
| taaaaccct  | cgagccca    | gccttatcag  | ctgggggtga  | gggaagactg  | gtctaggtgc  | 240  |
| tgctcctgaa | cttggtctct  | gagccatggc  | ttcccactaga | cactcagggtc | cctccagcta  | 300  |
| caaggtggcg | accatggcgg  | agaagtttga  | ctgccactac  | tgcagggatc  | cottgcaggg  | 360  |
| gaagaagtat | gtgcaaaagg  | atggccacca  | ctgctgctgt  | aaatgctttg  | acaagtctctg | 420  |
| tgccaaacac | tgtgtggaat  | gcgcgaagcc  | catcggtgog  | gactcccaag  | aggtgcaacta | 480  |
| taagaaccgc | ttctggcatg  | acacctgctt  | cogctgtgoc  | aaagtgccttc | accccttggc  | 540  |
| caatgagacc | tttgtggcca  | aggacaacaa  | gatcctgtgc  | aacaagtgc   | ccactcgagg  | 600  |
| ggactcccc  | aaagtgcagg  | ggtgcttcaa  | ggccattgtg  | gcaggagatc  | aaaacgtgga  | 660  |
| gtacaagggg | accgtctggc  | acaaagactg  | cttcaacctgt | agtaactgca  | agcaagtcat  | 720  |
| cgggactgga | agcttcttcc  | ctaaagggga  | ggacttctac  | tgcgtgactt  | gccaatgagac | 780  |
| caagtctgcc | aagcattggc  | tgaagtgc    | caaggccatc  | acatctggag  | gaatcactta  | 840  |
| ccaggatcag | cctggcatg   | cogattgctt  | tgtgtgtgtt  | acctgctcta  | agaagctggc  | 900  |
| tgggcagcgt | ttcaccgctg  | tggaggacca  | gtattactgc  | gtggattgct  | acaagaactt  | 960  |
| tgtggccaag | aagtgtgctg  | gatgcaagaa  | ccccatcact  | gggtttggta  | aaggtccagc  | 1020 |
| tgtgttgcc  | tatgaaggac  | aatcctggca  | cgactactgc  | ttccactgca  | aaaaatgctc  | 1080 |
| cgtgaatctg | gccaacaagc  | gctttgtttt  | ccaccaggag  | caagtgtatt  | gtcccgaactg | 1140 |
| tgccaaaaag | ctgtaaaactg | acaggggctc  | ctgtcctgta  | aaatggcatt  | tgaatctcgt  | 1200 |
| tctttgtgtc | cttactttct  | gccttatacc  | atcaataggg  | gaagagtggg  | ccttcccttc  | 1260 |
| tttaaagtct | tccttccgtc  | ttttctccca  | ttttacagta  | ttactcaaat  | aagggcacaci | 1320 |
| agtgatcata | ttagcattta  | gcaaaaaagca | accctgcagc  | aaagtgaatt  | tctgtccggc  | 1380 |
| tgcaatttta | aaatgaaaac  | ttaggtagat  | tgaactctct  | gcattgtttc  | catagagcag  | 1440 |
| aaaagtgtca | atcatattagc | cacttagtga  | tgtaaagcaag | aagcatagga  | gataaaacc   | 1500 |
| ccactgagat | gcctctcatg  | cctcagctgg  | gacccaccgt  | gtagacacac  | gacatgcaag  | 1560 |
| agttgcagcg | gctgctccaa  | ctcactgctt  | caccccggtt  | ctgtggagcc  | gggagaagg   | 1620 |
| accctacttg | accatggcat  | ggggttaact  | ttcctcatca  | ggactctggc  | cct         | 1673 |

## (2) INFORMATION ON SEQ ID NO. 14:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1593 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

ggggccaggga cggccgccgg cgccggagtgg ctgccctcg cggggacact cagagcccg 60
tgggcggggag gaaggcgga tgcccagac ggtgatcctc ccgggcccctg cgccctgggg 120
cttcaggctc tcagggggca tagacttcaa ccagcccttg gtcatcacc gattacacc 180
aggaagcaag cgggcactgc caacctgtgt cctggagatg tcatcctggc tattgacggc 240
tttgggacag agtccatgac tcatgtgat gcgcaggaca ggattaaagc agcagctcac 300
cagctgtgtc tcaaaattga caggggagaa actcacttat ggtctccaca agtatctgaa 360
gatgggaaag cccatccctt caaaatcaac ttgaatcag aaccacagga attcaaaacc 420
attgttaccc cgcacacacag aaggggccag cctttgtgtg cagctgcaca cattgatgac 480
aaaagacagg tagtgagcgc ttccataaac tcgcccaattg ggctctattc aactagcaat 540
atacaagatg cgcttcacgg acagctcgcg ggtctcattc ctactctacc tcaaaacgag 600
cccacagcct cggtgcccccc cgagtccggc gtgtaccgga tgctccacga caatcggaat 660
gagccacacac agcctcgcca gtccggctcc tccagagtgc tccagggaat ggtgacgat 720
ggctctgatg accgtccggc tggaaacggc agtgtgagag ctccggtgac gaaagtccat 780
ggcgtctcag cgccgggcaca gaggatgcgg ctctgtgaca aatgtgggag tggcatagtt 840
ggtgtgtgtg tgaaggcgcg ggataagtac cggcacccctg agtgcttgt gtgtgccgcg 900
tgcaacctca acctcaagca aaagggtcac ttcttcatag aaggggagct gactgcgcaa 960
accacgcaaa gagcccgcac aaagcccccga gagggctatg acacggtcac tctgtatccc1020
aaagcttaag tctctgcagg cgtggcacgc acgcacgcac ccaccacgac gcacttacac1080
gagaagacat tcatggcttt gggcagaagg attgtgcaga ttgtcaactc caaatctaaal1140
gtcaaggctt tagaccttta tctattgttt tattgaggaa aaggaatggg aggcaaatgc1200

ctgctatgtg aaaaaaacat acacttagct atgttttgca actccttttg gggctagcaal1260
taatgatatt taaagcaata attttttgta tgcatactc cacaatttac atgtatat1320
cagccatcaa acacataaac atcaagata ttgaaggact ctaattgtct ttcccttgacal1380
agttgatttt gcaattgtgg taaatagcaa atacaactct tgtattccaa cataactctgc1440
agttgtctgt atgtgtttta actattacag tgcattgttag ggagaaattc cctgaatttc1500
tttagttttg tattcaaaaca attatgccac tgcattgcaac aaacataata aatacataaal1560
agattctaaa aataaaaaaa aaaaaaaaaa aaa
1593

```

## (2) INFORMATION ON SEQ ID NO. 17:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1722 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

cattgttttcg caaaatccca ggcagcatgg acctcagttc tctctgggta cttctgcccc 60
tagtcacccat ggcctggggc cagtatggcg attatggata cccataccag cagtatcatg 120
actacacgga tgatgggtgg gtgaatttga accggcaagg ctccagctac cagtgtcccc 180
aggggagcag gatagtgggc gtgaggagca tcttcagcaa gaaggaaagt tctgacagac 240
aatggaaacta cgcctgcacg cccacaccac agagcctcgg ggaacccacg gagtgtcgtg 300
gggaggagat caacagggct ggcattgaaat ggtaccagac gtgctccaac aatgggctgg 360
tggcaggatt ccagagcccg tacttcgagt cagtgtcggg tcgggagtggt cagttttact 420
gttgctcgcta cagcaagagg tgcccataat cctgctggct aacaacagaa tatccaggct 480
actatggtga ggaattggac atgatttcct acaattatga ttactatatc cgaggagcaa 540
caaccagtgt tctctgcagt gaaagggatc gccactggaa gttcataatg tgccggatga 600
ctgaatacga ctgtgaattt gcaaatgttt agatttgcca cataccaaat ctgggtgaaa 660
ggaaaggggc cggggacagg aggggtgcca catatgttaa catcagtgg atctccata 720
gaagtttctg ctgctctctt tcttctctcc tgagctggta actgcaatgc caacttctgt 780
ggcctttctg actagatca cacttctaat aaaatccaca attaaacctat gttttctcat 840
tttcacatgt ttcatagcaa ctgctttata tgactgatga tggcttccct gcacaccaca 900
tatacagtcg ccatgcttac agccgggctt ctggagcacc agctgcagcc tggctactgc 960
tttttactgc agaatgaact gcaagtccag catagtggag gggagaggca gaactggagg 1020
agaggtgcag tgaaggttct ctacagctaa gctgttttga atgatactga ggttccccac 1080
caaaagcagg ctttctgccc tgagggaact cttcccactc cctgtctcca catgagccat 1140
gcattgcttg caatcccaag gcagagctct ttgctccagg agtgaggaga ctggggaggt 1200
aaatggggaa atgggaaggt ttggaggcag agctgaaaac aggggttgga ggatttctgt 1260
aaattagaaga caaacggttg cataccagat aaggaaaaat agtgccaggg ccaggggaaac 1320
ccgtgaggat cacttccaaa tgagattaaa aacaaggaa gtacagagatg 1380
ggattccagt tgggaacttg tggggatgag agtgaccagg ttgaactcgg aagtgaaaaa 1440

aggagtttga gtcactggca cctagaagcc tgcccacgat tcttaggaag gctggcagac 1500
accctggaa cctggggagc tactggcaaa ctctcctgga ttgggctga ttttttgggt 1560
gggaaaggct gcctggggga tcaactttcc ttctgtgtgt ggctcagga ttcttctgca 1620
gagatggcgc tatctttctc cctcctgtga tgtctgtctc caaccattt gtactcttca 1680
ttacaaaaa aataaaaaa ttaacgttca ctatgctgaa aa 1722

```

## (2) INFORMATION ON SEQ ID NO. 18:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1648 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

tgaccaagaa acagggccta aggatcattt tctcggatgc atcacggctc atcttcocggc 60
tcagttcctc cagtggtgtg cggggccacc tgcagactgt acgcagagag ctacgagagg 120
gatcccagcg gccatgacca ggagccacag gcagtgctga gccctctcat agccatcgca 180
ctgaaaaaat cccagattca tgagagaact ggccggaggg gacccactgt catcacctga 240
atagaggaaa gatcactcac caggggccaaa gagagtgtct agcggggagt gcttcactga 300
tgccttcttg ctacctgttt gtgcctctta tgactttgga aaaacaaaag atattttgtct 360
tttgggggat agaggggtgg tgggaaaaga aaaaaatcc atttggtttt gggtttgtcc 420
tattcctcca aatgcagcag gccctttagt tgtctgttaa agctgcacta taatttggta 480
tctacatttt atcacacaaa ggaacctccc cttttgacaa caactgggct aggcagctgt 540
taatcacaca atttgtgat cacttgtgcc aagttagaaa atgttctaaa atcacagag 600
agaacagtg cagaatgaaa ctgaccttaa gtcccagggt cccctgggca ggcagaagga 660
gacactcccc gcatggagga gggtttatct ttctatccta ggctcaggtc acaatggggg 720
aagggtttat tatagaactc coaacagccc acctcactcc tgcccaccca ccgatggccc 780
tgctcccccc atcccattccc caacatccct gtaccacctt ctctcacatc ttctaaagct 840
ttgtacaaa cacaatgggt cacttccaac aaaatatatc aatagggtgt ttccctctct 900
attttgtaaa tagtattatt ttagctatta agctggatac ctctcttcaa attcagccat 960
tcagttgtaa agttgggaag aagtttcttg acaagactct gcaattaaat gcttaaaaatt 1020
tggaggggat ccttccctga ttacatcaag tatgttggtg catgggttta tacaagtctc 1080
tcttgagaag gcaaaaagac caccatgtgt gagagctctt tgacttgggc aataggggcc 1140
tatcttaagt cacttgtttg gacacatttc tgatcttatt tgtaaaaggct gcaaaaggag 1200
aggatgaat gctgtaaaag taggaaatga agtgggaagt ggaagaaaaa gtaagtgtgt 1260
gtcacgctat gggccagatg gtggagggga gggtggggag ccctggccgc aagcagagtgt 1320
tcacagctgg ctttctctac ttgggaaaaa ggtactgccc gtctagcagc ctctctgtat 1380
ctcagccagg acaccacgag cgtgggaacct gtttgtgtct gttttgtctc cttgggaaag 1440
gcacagtcac taacctctgc atttgcggaa atgacctggg gcactttgac tgttaagcaa 1500
tgcgcttatt ctgtagtcaa gttttagtga agcaaggaaa catctccagt aaggtattgt 1560
ttcccaattt ctgtctgtgc ttctgtcaga aacttgc tagcttttagt gcccaataaa 1620

```

aagaaatccc taatttcaac cttaaaaa

1648



## (2) INFORMATION ON SEQ ID NO. 20:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1610 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

gcgcgctgat  tggacgcgtg  gggcgaggcg  gaggagagcc  gtgcgcacgg  cgtatgtggg  60
gccgtgtgca  gaaccgcgtg  tggcgcgagg  aaggaccctc  aaaataaaca  gcctctacct  120
tgcgagccgt  cttcccccag  cctgcgtccg  agtctccgcc  gctgcggggc  cgctccgacg  180
cggaagatct  gactgcagcc  atgagcagca  atgagtgttt  caagtgtgga  cgactctggc  240
actgggcccc  ggaatgtcct  actggtggag  gccgtgtgtg  tggaaatgag  agccgtggca  300
gaggtttcca  gttttgttcc  tcgtctcttc  cagatatttg  ttatcgctgt  ggtgagtcgt  360
gtcatcttgc  caaggattgt  gatcttcagg  aggatgcctg  ctataactgc  ggtagaggtg  420
gccacattgc  caaggactgc  aaggagccca  agagagagcg  agagcaatgc  tgctacaact  480
gtggcaaac  aggccatctg  gtcgtgtact  gcgaccatgc  agatgagcag  aaatgctatt  540
cttgtggaga  attcgggacac  attcaaaaag  actgcaccaa  agtgaagtgc  tataggtgtg  600
gtgaaactgg  tcatgtgacc  atcaactgca  gcaagacaag  tgaagtcaac  tgttacccgt  660
gtggcgagtc  agggcacctt  gcacgggaat  gcacaattga  ggctacagcc  taattatttt  720
cctttgtcgc  cctctctttt  tctgattgat  ggttgtatta  tttctctga  atcctcttca  780
ctggccaaag  gttggcaga  agaggcgaat  ccagggccag  tgagctttac  ttgcccgtga  840
aaaggaggaa  aggggtggaa  aaaaaccgac  tttctgcatt  taactacaaa  aaaagtttat  900
gtttagtttg  gttagaggtg  tatgtataat  gctttgttaa  agaaccocct  ttccgtgcca  960
ctggtgaata  gggattgatg  aatgggaaga  gttgagtcag  accagtaagc  ccgtccctggg  1020
ttccttgaac  atgttcccat  gtaggaggtg  aaaccaattc  tggaaagtgc  tatgaacttc  1080
cataaataac  ttttaatttt  gtataatgat  ggtcttggat  tgtctgacct  cagtagctat  1140
taaataacat  caagtaacat  ctgtatcagg  cctacatag  aacatacagt  tgagtgaggag  1200
taaacaaaaa  gataaacatg  cgtgttaatg  gctgttcgag  agaaatcgga  ataaaagcct  1260
aaacaggaaac  aacttcacat  cagtgttgat  gttggacaca  tagatggtga  tggcaaaggt  1320
ttagaacata  ttaattttcaa  agactaaatc  taaaaccocag  agtaaacatc  aatgctcagag  1380
gttagcatca  tttggagcca  ttccaggaat  gcagagaaat  gcattttcac  agaaatcaag  1440
atgttatttt  tgtatactac  atcaacttag  caactgtgtt  tcatttgtgt  taatcagttt  1500
ttaaaagtca  gctggaaaga  gcaactgaag  tctagaaaaa  tagaaaagta  attttaacct  1560
attccaataa  agctggaggga  ggaaggggaa  aaaaaaaaaa  aaaaaaaaaa  1610

```

## (2) INFORMATION ON SEQ ID NO. 21:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1108 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

ggaggcgccg ggagagtagg gtgctgtggt ctgagctaga ggggtgaagct ggcggacagg 60
aggatggcg tatgcaggtg atagactaga gaacaagacc tctgtctccg tagcatcctg 120
ggcgagcagt ctgaatgccca gaatggataa ccgttttgcg acagcatttg taattgcttg 180
tgtgtcttagc ctcattttcca ccatctacat ggcagcctcc attggcacag acttctggta 240
tgaatatcga agtcaccgttc aagaaaattc cagtgtattg aataaaagca tctgggatga 300
attcatttagt gatgaggcag atgaaaagac ttataatgat gcacttttcc gatacaatgg 360
cacagtggga ttgtggagac ggtgtatcac cataccctaa aacatgcatt ggtatagccc 420
acgagaaaag acagagtcac ttgatgtggt cacaataatgt gtgagtttca cactaaatga 480
gcagttcacg gagaaatttg ttgatcccg aaaccacaat agcgggattg atctccttag 540
gacctatcct tggcgacttt agttcctttt acctttttgt agtttaggtt tgatgtgctt 600
tggggccttg atcggaacttt gtgcttgcat ttgcgaagc ttatatccca ccattggcac 660
gggcattctc catctccttg cagggtctgtg tacactgggc tcagtaagtt gttatgttgc 720
tggaaattgaa ctactccacc agaaactaga gctccctgac aatgtatccg gtgaatttgg 780
atggtccttc tgccctgctt gtgtctctgc tcccttacag ttcatggctt ctgctctctt 840
catctgggct gctcacacca accggaaaaga gtacacctta atgaaggcat atcggtgggc 900
atgagcaaga aactgcctgc tttaacaattg ccaattttat ttttttaaaa taatactgat 960
attttcccca cctctcaatt gttttaattt ttaaatggg ggatatacca ttttattatg 1020
gaaaatccat ttaatttata caccatccac cactaaatcc ccccttaat accccctaaa 1080
atttaagggg ggttacctta aagcgatg

```

## (2) INFORMATION ON SEQ ID NO. 22:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 675 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

agggaaagag agagagagagc ctagacgaac acaatcacat gttttctttg ctgttcctcc 60
cgggatgggc ctgttttggg gtttgggact ctgaaccoga gcgggggttc ttgccttgac120
tttgatcctg gtccctaaat gcctttcccc actccccctc cgtgggttca ggggccaaag180
ggccccctcc cagagcacgg gcagcacctg ctctggacc cctgtgtgcc agcctctgca240
gacgcagctg gtgggagggg gcatggattt ggagggtggag aagtcactcc tggctcctgg300
aggggggtgg ctgtgtgctt agttcagtg gactcgggga ttggtgaggg cggacagggt360
tctgagggct ccctagcctt ctttgtaaat tcacacgaga tagtccaggg ctttccagcg420
cccagcttgg atgataatcc tegtgtcccc cactctaagg cctccttgag attttlttgg480
ggtctaccac gtccctctgcc tgtctccagg tggtagagga gatgtggttc ctgtccctct540
cctgggtccc tagggggccc cagggccctt ccctgtagct ttagctgacc ccattggtgt600
gggtgtgggg tctgtgcgag tgctcaggta agcttggggg ctccaggtaa gcggtcccga660
agaacggggg gggag

```

675

## (2) INFORMATION ON SEQ ID NO. 23:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 350 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

agcagagc aa ggtgggtt cgtcctctgg cagaacctcg gctctcagga ggtccttgtt 60
ccagggaaca gctgcttctc tgggggctgg ggcttctaac ttccctggca gccctctggc120
actaaccacg ctggaaca ca ggggaacaaa cggcctggag tgccaaaccc ttctgtctct180
ttttttccag aaaaacgggg gcaatggctg ttgaggagcc catttgggaa gaactggtgc240

ctctaatggg gcaaatggat tctgcagggg gctgcagttg ggcagggaaa attccttcaa300
acaagggggt ccaccccaaac ccaggccccg gcttcaaatg gccagaaaaa 350

```

(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 746 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

ccccccctcc tccggttttt ttttttttat ttaagaaat ttattttctac ttctacagca 60
gaaatacggg aatggtacag gtttgggcaa atcatacttt atgaaatgga tcttcatacc120
acâtcctttt taatacaggc acgttataac ataattcctg gattttcaaa atccagccaa180
cacggatacc tctgctactc tgttttggcc ttcatactg cttcctcttt cagacgagct240
ttctttttct agttcaagct tgttaaagtc tegtgtcttt gggcagcctt cttgccctca300
ataaccaatga agatgcaccc taccaccgtc agggcaatca ttagatagct gatcttcaact360
cgcactctgt tctttgcagc atcaagcctc tccaaagaga cagtctctgg gatttcactct420
tcttttttga agcgacctga ccataatgagg atctttttct gccaatccgt aggtttgtgt480
aaaggcactc tgttgttaagt gggggatgga gctccgggac tttcctgtgg ttttgtgcaa540
aatccattta ttctcttcaa atcagagctt ctggtaagcc ttagagatga gaaaacatct600
ctttcacata acctaaaaaa gcttctctgt gccaggcgca gaccgctgag gctcccatg660
gccacttgct actccgcca ccagcgcaga acttcgccgg ggacggtggc gctggtgagc720
tcaatgtcac ccagcgcttg agtggg 746

```

## (2) INFORMATION ON SEQ ID NO. 25:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 217 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

agtgtatggc agcaaatgag ggaatcatac tctcagttta ttgatgatta ttcactctca 60
gatggaggag ttatcccgtc agccacttca gtttgccttt aaaacaggag cccacaggac120
ccaagggaact attaaggagg accaggaacc taggtttttt ctttcaaaaa attggccctal180
gcccaataaa tgaaggaaaa aattaggcac ctttttt 217

```

## (2) INFORMATION ON SEQ ID NO. 26:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 392 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gcgggacccgg cggtctccac tgatcttttc caaggctgta cagacatggc ggcggctttt 60
cggaaggcgg ctaagtcocg gcagcgggaa cacagagagc gaagcagtga ctacgtaaa120
aaacaagaat acctcaaagc tcttcgggaag aaggctcttg aaaaaaatcc agatgaattc180
tactacaaaa tgactcgggt taaactccag ggtggagtac atattattaa ggagactaag240
gaagaagtaa ccccaagaaca actaaagctg atgagaactt caggacgtca aatatatagg300
aagggaagag ggtgcagaag ctaagaaaaat cgaagactaa aatcagggcc catctgcggg360
ttgcagggga ggcaggaaaa ggttggtttt tt                               392

```

## (2) INFORMATION ON SEQ ID NO. 27:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1796 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

cggctcgaac gtattagtgt ttcttaattt ttttccagc aaaaatgga tcttttaaga 60
agaatttgag aagcaaaaca ttacatgtca tgtcaagggt gtagcagatt ccatttggct 120
tcaatattgc cacaataccc agggattaat gctgccacag gggggcaact tttatttgtc 180
ttacttccta ccccttccct gtctgccttc ttaactcag ttaagtgtgt ctgtttggga 240
cctggaaaag aaccocaaaga aaacctgagt ggacagggtc atttctggaa tgcagaaaaa 300
attttaaagg ctatgatttt agaatactct caactagcat tctttccatt gatttgaagg 360
ggaaattaac tattataatc tcttgaatcc aaaactggat attaagaact ttccccctta 420
ctaaagttta gacttttgtc atgtggtgag tcaataaaga ccattttgat tgtaaaacct 480
aaaaatgttc agcaagttag ccacagtctc ggctaacag cagacttgcg gttttcactt 540
ggatatcctg agttgggttg ctaaccttaa tttctatgat gttttctaaa atgaaaactg 600
ataaagtaga ccaccagctg caccgtgttt tctgtaaaag tattgttagt aagtggccaa 660
gagacttgag gaaaaatacag attttttgtt taccttggct ttgttttaag tcttaaaaaa 720
taaagataaa cattataatg tagaatacag atgggacata gtccctgttaa gcttcccttg 780
aaaaatgttt aaattatttg gaagctttta aaagacacta aattgtactc taaaagacac 840
taaatgttac taattgtaca aaggtcaagc caattttatg aaacagtcct acagagtaat 900
atatgtgatg cagtgttaaga aggaaaaatac tcactctcaa cattatggta ataacattta 960
gctcttagg agttggagca gggggatggg taattacaga ttgacagact atagaaaagag 1020
tttcattttt ttgtgacccc acagagtctc aaatttttat ttcaactacct gctagagcct 1080
actgtgaaat cactgtccca tatttgccag tggaggaaat gggcatagag tagagaaatag 1140
cttcatatgt ttacacgttt gcatagacta cacacatgtc atgcgtttat ggcaggttagc 1200
tggattttat tccccaaagt aataatgttg aagtatgggt ctcatcattc ccatacacag 1260
aaacacaaaa cactttgatc ataaactttt ttcttcagaa gccaaaacta cttgcagaat 1320
aatagagcca ctggtttaat gtttctcaca gatagggttt agtgaagct agtattctgt 1380
gtgttcgtag aaatgattca atacctgcag ctgggtgaatt aggaattgta tttgtgcct 1440
tttttatatt agatgaggtg caaaaaattt aatgctagtc agtatgcacc accacagga 1500
agttagatcc cattagcact tgaaaactaca gctttggaaa cttaggctaa gtttaatttg 1560
atttgttact tgattccact actgaccttt tcttttgttt gaagtgccta tcagcataat 1620
gagctaaagt tcatgcatat ttgtgaagaa acaccctttt tggtcocctt tgggacagag 1680
aggtaactct tgatctttat gaatgacagg ttactgtttt gccttattgc ttaactaat 1740
gtagtgaat aaagcagaca aagcttgaaa aaaaaaaaaa aaaaaaaaaa tcgacg 1796

```

## (2) INFORMATION ON SEQ ID NO. 29:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2927 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

|             |             |             |             |             |             |      |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| gaagaaaaag  | aggagaaaa   | aggtaggagg  | aaataaagg   | aggagagaag  | cacagtgaag  | 60   |
| gaaaaaaaaa  | gtcccttttc  | gacatcacat  | tcctgtgrrt  | tcctccagcc  | tggaataaat  | 120  |
| attaatccca  | gtccttttac  | gcccggaaac  | aaagagacta  | agccagacta  | tgggggaaaag | 180  |
| ggagataaga  | aggatccctg  | aacttttaag  | agggaagag   | tgagatttcag | aaatccgccag | 240  |
| gactggactt  | taagggaagt  | cctgtgtcag  | cacaaggagc  | tgccacacac  | agcacacaga  | 300  |
| gaccaggagc  | aaactgcaga  | caaatggaga  | tacaaagact  | tagaaggaca  | gtccctttca  | 360  |
| ccctcatccta | ctgtgtccaga | aggtaaaaag  | acacagccag  | aaagaaaagc  | catcggtctca | 420  |
| gtcttcagat  | caggacaggc  | tgtggatctg  | gtgcgggtact | ctgaagactg  | ctctgcagcg  | 480  |
| acaccccttt  | tgtattgtct  | acccctggta  | aagagagaga  | gggctggggag | gaaaagttagt | 540  |
| tcactctagg  | aactgtccctg | ggaaccaaac  | ttctgatttc  | ttttgcaacc  | ctctgcatttc | 600  |
| catctctatg  | agccaccatt  | ggattacaca  | atgacatgga  | gaatggggacc | ccgttttcaat | 660  |
| atgctgttgg  | ccatgtgggt  | agtgtgtgga  | tcagaacccc  | accccatatg  | cactatttaga | 720  |
| ggcagccacg  | gaggacggaa  | agtgcctttg  | gtttctccgg  | acagcagtag  | gccagctcgg  | 780  |
| ttcttgagcg  | acactgggag  | gtctccggga  | attgagagat  | ccactcttga  | ggaaacaaac  | 840  |
| cttcagagctc | tcacagagaag | gaggagtgtg  | cccgtgttga  | gactagctgc  | cccaacagag  | 900  |
| ccgcccagccc | gtctgggacat | caatggggcc  | gcccgtgagac | ctgagcaaaag | accagcagcc  | 960  |
| aggggctctc  | cgctggagat  | gatcagagat  | gaggggtccct | cagctcgcttc | agaaagtgtg  | 1020 |
| cgtttccctt  | cggtgtccag  | ctctcccaac  | atccttgcca  | gctttgcagcg | gaagaaacaga | 1080 |
| gtatgggtcca | tcacagcccc  | tcactgcctcg | gaaggcttact | accgcctcat  | gatgagcctg  | 1140 |
| atgtagggag  | atgtgtactg  | tgagctggcg  | gagaggcaca  | tcacaacagat | tgtgtctcttc | 1200 |
| caccagggag  | gtgaggaagg  | aggcaagggtg | agaaggatca  | ccgcaggggg  | ccagatccctg | 1260 |
| gagcgagccc  | tggaccctag  | ccctcatccct | aagctgtaga  | gcttctctgaa | gcttgagaaag | 1320 |
| ggcaagtttg  | gcattggtct  | gtcgaagaag  | acgctgcagg  | tgaggaggcg  | ctatccatat  | 1380 |
| cccgttaggc  | tggaagccat  | gtacgaggtc  | atcgaccaag  | gccccatccg  | taggatcgag  | 1440 |
| aagatcagcg  | agaaggcctt  | tgtccagaaa  | tgtaaagcct  | ctggtgtaga  | gggccaaggtg | 1500 |
| gtggcggagg  | ggaatgacgg  | tgagggggga  | gcagggaagc  | caagcctggg  | cagcgagaaag | 1560 |
| aagaaagagg  | acccaagagg  | agcacaagtc  | ccaccaacca  | gagagagtgc  | ggtgaaaggtc | 1620 |
| ctgagaaaaa  | tggccgcacc  | tgccccagct  | ttgccccaac  | ctccctcaac  | ccccagagcc  | 1680 |
| accacccctc  | ctcctgcccc  | agccacaaca  | gtgactcggt  | ccacgtcccg  | ggcggttaaca | 1740 |
| gttgctgcga  | gacctatgac  | caccactgcc  | tttcccacca  | cgcagaggcc  | ctggagcccc  | 1800 |
| tcacccctcc  | acaggcccccc | tacaaccact  | gaggtgatca  | ctgccaggag  | accctcagtt  | 1860 |
| tcagagaaat  | tttaccctcc  | atcccggaa   | gatcagcaca  | gggagaggcc  | acagacaacc  | 1920 |
| aggagcccca  | gcaggccac   | cagcttgag   | agcttcacaa  | atgccctcc   | caccaccatt  | 1980 |
| tcagaaacca  | gcacaaggcg  | tgctggccca  | ggcgttttcc  | gggacaaccg  | catggacagg  | 2040 |
| cgggaaacatg | gcacccgaga  | cccaaatgtg  | gtgccaggct  | ctcccaagcc  | agcaaaaggag | 2100 |
| aaacccctcca | aaaaagaagg  | ccaggacaaa  | attcttagta  | atgagtagta  | ggagaaagtag | 2160 |
| gacctcagcc  | ggcctactgc  | ctctcagctg  | gaggacgagc  | tgcaggtggg  | gaatgttccc  | 2220 |
| cttaaaaaag  | caaaaggagt  | taaaaagcat  | gaaaagcttg  | agaaaccaga  | gaaggagaaag | 2280 |
| aaaaaaaaga  | tgaaagaatga | gaacgcagac  | aagttactta  | agagtgaaaa  | gcaaatgaag  | 2340 |
| aagctctgag  | aaaagagcaa  | gcaagagaaa  | gagaagagca  | agaagaaaaa  | aggaggtaaa  | 2400 |
| acgaacagag  | atggctatca  | gaaacccacc  | aacaaacact  | tcacgcagag  | tcccaagaag  | 2460 |
| ctagtgccgc  | acctgctggg  | gtcctttgaa  | ggcaaacgaa  | gactcctctc  | gatcaactgt  | 2520 |
| cccaaggctg  | agaaacaatat | gtatgtgcga  | caacgtgatg  | aatatctgga  | aagtctctgc  | 2580 |
| aagatggcta  | ccaggaaaaat | ctctgtgata  | accatctctg  | gocctgtcaa  | caacagcacc  | 2640 |
| atgaaaaatg  | accactttca  | gctagataat  | gagaagccca  | tgcgagtggg  | ggatgtgaa   | 2700 |
| gacttggttg  | acagcgttct  | catcagcgag  | ctgaggaaag  | agtacggaat  | gacctcaaat  | 2760 |
| gactttctca  | tggtgtctaac | agatgtggat  | ctgagagtca  | agcaatacta  | tgaggtacca  | 2820 |
| ataacaatga  | agtcgtgtgt  | tgactctgac  | gataacttcc  | agtcccaagt  | caaaagatatg | 2880 |
| gagaaccaga  | agaggggggt  | tttttttgaa  | gggggaaaaa  | cgcccccc    |             | 2927 |

## (2) INFORMATION ON SEQ ID NO. 30:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 743 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

tccgtggggc tttaaaaaat ggttggtgggt gtgtggggtt ttttgagggt ggagaggatg 60
tgtgaaaaatc ttttccaggg aaatggggttc gctgcagagg taaggatgtg ttcctgtatc120
gatctgcaga caccagaag gtgggtgcac actgcatgct tgggggtgcc aagggtatcg180
agacctccaa cactactgtc tgaagctcgt gccgtggcc atggccocctc tgccaagcct240
gtgtgcgatg ccccttgggtc tttagtgcga gaagcctagg ctccagaagca cagcagcgcc300
atctttccgt ttcagggggt gtgatgaagg ccaaggaaaa acatttatct ttactatttt360
acctacgtat aaagttttag ttccattgggt gtgcgaatac ccccttttat cactttttaa420
tttgacattt attttttttc ttccatgctt gttctctgga catttgggga tgtgagtggt480
agagctgggt agagaggagt caggcgccct tcccaccgat ggtccctggcc tccacctgcc540
ctctcttccc tgccctgatc ccgctttcca atttgccctt cagagaactt aagtcaggga600
gagttgaaat tcacaggcca gggcacatct tttatttatt tcattatggt ggccaacaga660
acttgattgt aaataataat aaagaaatct gttatatact ttccaaaatc caaaaaaaag720
tagggagggt aagaaaaagg gcc

```

## (2) INFORMATION ON SEQ ID NO. 31:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1667 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

agagccaata gcatgggggt tacaaggcaa agatagtcac tcattcaaca catattcata 60
gagctccctc tctgtgccag acactgttct ggaagatagc tagatgaaaa tctttgcact 120
cacagagctt acatgccagt gagtgaagat cgatgataaa taaagcaaat gcatacatatg 180
ttcacatttg ataagtatat gccaaaaaat gaagccggga aggaggacaa ggcccatggg 240
tgggtgttga ggtttttaaa gtgtggtcag gaaaggcccc actgataagg taacatttga 300
gcaagtctga aaaaggccaag gggatctttg gggctaactt cgggatccct gcactttatg 360
taagaatgta aacctggagt ctcatttaag aatgatcagc aatacgttta gaacatatga 420
actgaatgaa atggacattt tttcttaatt tacgtataaa tccatatgat tatacataaa 480
gttctgatgc attaataaaa gcagccaaat agggccaaag agaaaaataa caggactctg 540
tactggacct aactttatca ttaattaggt aatattttcc tcatttcttt actgctgcc 600
ttttctcac cagtattcca gagatggcca tagctcata ctctaccacc aagaacctaa 660
aagggaattag aatacacgag aattggcctc agtgaagagc ttaaaattgt tctcctcgta 720
gaactggact attgatcatt accacgtgac gttggctcta ttactttctg ttcccaatgt 780
cctctagtgt gtttgaaaat gttaaaaaat ccttaaaatc taaatcatat aatcagaatt 840
ctatagtgtc caactctatc tgaataagatc atttggaaga ctttagactc tatataattt 900
aaaaaggaata tttattagcc atatgcagaa tttctaata tgatatgtga cagcttctaa 960
ttcacttttc agatcagtg ttgaaatggc aattatcagt gttggattta gttccaaacta 1020
cttgatttac aaaaatgtac atttagagaa ggttaaaaga aacagtgaga aatgtaaacaa 1080
ttcaaaatga taattgaatc tctcagttgt gggaaataat atcagagaca tgcactgaa 1140
aatgtctcac ctttcattct tttttcttaa ttcataaagt tatctgttag aatttgatga 1200
gacctctcta gtcatttcca actggggcgg tgcgtgcacc gaatggtgtt tgagagtgtt 1260
ggggctaggg cacatttttg gttgtcacag caactggggt ggcatttgtc gccagtgcc 1320
aggaatagta acattatgaa tgccagggac agtgtgtcca gtaaagctct ccattccaaa 1380
ggggcagggc acgggtgtct acgctgttaa tccagcactt ttgggaggcc aaggtggcg 1440
gatcacctga tgtcaggggt tcgagaccag cctggccaac atgggtgaac cctgtgtcta 1500
ctaaaaatac aaaaattggc tgggtgtgtt gtcacatgcc agtaacccca gctactagg 1560
aggctgaggc aggagaatca cttgaacccg ggaggcagag gttgcagtga gctgagattg 1620
caccactaca ctccagcctg gatgacagag tgagacttca tctcaaa 1667

```

## (2) INFORMATION ON SEQ ID NO. 32:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 249 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

cgtggtaggc  acctcatcag  tgtttactga  ttgaaaacat  tgttgactgt  ggcttctatc  60
agagtgtcta  ccttttacag  ctctgacctt  acctcattta  atttgctgct  tttaatctac  120
gggggctgag  aatttgtgaa  accagtgttg  ttagaagtgt  atataatctg  aatcaataag  180
ctctgaatgg  gggacaagaa  acgctcttat  agcacaaaga  tgcattggact  tcatgacagc  240
tcttttggt

```

## (2) INFORMATION ON SEQ ID NO. 33:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1246 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```

aatggaagtg taattaccgg ggcccacctt gagacggaaa aaaatttgga aaacgaaact 60
aaaaatgggt ggggtgaatt tctacccaaa gtccagcggt ggtgggtgca ctggcacaga 120
atactaaact gagtgtgact attttcaatg caacaaatga aaaaacaaaa tgtgcctgtt 180
taaagcactc agtagagggc tgatgaaact aatttttttt cttttaagac atgcactctt 240
gagtctctca gtaactgagt gttgttttag acagcacaaag aagggggtgag agtgcgtctc 300
ctagccttaa tegtgggaggg tagtttcagt cactcatcgg ctttcaattt tgtgcagaaa 360

tattagaaaa cctcattgat caattttatg tatttgaata tcagcaaatt gaaatttttc 420
ataattatca ttaattttgt accacatcca gtgtcatgct tactccttag agttcagatg 480
aattcttaaa attaaaaaaa aactccatag tactaatttt gtttctttat atagtgttgg 540
tttgatatta gtgtttgcaa ttgtattaaa gtcaaaagct gatttttatg gcatacacaa 600
gaatgccact ttttctttta ttccatacca ataattttaa gattgatgat ctaaaaacaa 660
tttgcaacgc actaaagcat gagctacttt catctaaacc tgtaaaaata tgaaagattt 720
ttatattttt tcaactgggaa gaaattcttc ctggatgaaa ttacaaatat gtgtagaata 780
tatttaataa aagactttata aaatacctaa ctacaggact taaaaatag attggcgctg 840
agtataatga acaatattcc atataataaa gtttagcctt tataaaaaatg aagttgcagg 900
ctgacattac attctgtact tactaagtgt caacagccct tacaacacatt aaatgtaaaat 960
ggtttcaaat ggtcagcggt gtttaaatgt aatcatgtta ttttattcat tgttaatgct 1020
ttgatgaaaa ggcttttatat gcagtagatc tacgaaaata ttgttcatac tgatcagaat 1080
taaatttgta tagagcagag ttttaaaatg aatgtaaaata gcactaaacg ttttctttct 1140
gcaacctgta ctacagatt ctctctgtaa actaaataaa aaaaaaatga tagtgcaaaa 1200
aaaaaaaaaa aaaaaaaagag acggagagag gagaaagagg gcgtgg 1246

```

## (2) INFORMATION ON SEQ ID NO. 34:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 215 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

gggaagcatt ttggatatga tgcaggaaat ctcttcctgg agtcaaaagt tcccaagagg 60
tgctgtatatt ttaagaaatg gagtttatatt aaataatagt taagctttgt cccatgttgg 120
ccgggcaact tttttcaatg gtgcttatta gaagaaagtgt tttcatctgg tcaatttaag 180
gaaataaaa taggaaatg agaggggggg agaga 215

```

## (2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 734 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

gctgcgcggg gcttggggct cggcgctcggg ccccggggga tgtggagagc tggcagcatg 60
tcggcccgagc tgggagtcgg gtgcgcattg cgggcgggtga acgagcgcgt gcagcaggct120
gtggcgcgccg ggcgcgcggga tctcccagcc atccagcccc ggctagtggc ggtcagcaaa180
accaaaacctg cagacatggt gatcgaggcc tatggacatg ggcagcgcac ttttggcgag240
aactacgttc aggaactgct agaaaaagca toaaatccca aaattctgtc tttgtgtcct300
gagatcaaat ggcacttcct tggccacctc cagaacaaaa atgtcaacaa attgatggct360
gtccccaatc tcttctatgct ggaaacagtg gattctgtga agttggcaga caaagtgaac420
agttcctggc agagaaaaag ttctcctgaa aggtttaaagg ttatggtcca gattaacacc480
agcggagaag agagttaaaca tggccttcca ccttcagaga ccatagccat cgtggagcac540
ataaacgccca agtgtctctaa cctggagttt gtggggctga tgacctagag aagcctttgg600
catgatctta gtcaaggacc aaatccagac ttccagctgt tattgtcgtt ccgggaagag660
actgtggtta aaagctgaac atccctgctg aacaggttga gctgatcatg ggcatgtccg720
tctgtaaaact gcaa

```

734

## (2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 314 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gctgctgggg agccactgaa ccaaccggag acccgctggt cccacgtgaa gcagctgtcc 60
tggtgtggag gtacagagct agaccagcac tggtcctctc agccctctgg tagcctctgc120
tgcaactgaa ctggcagctt ttgccgctgc ctttagctct gcatgtatgc gccctgaagg180
ttctgctct ctgttttgga atcgcttcc cctcctcatg tttggggacc tgcaagggtg240
tgaggcacgt gagggcatcg ccatgcgtat ttacaggcc tctttctctg gactgtcttc300
aaagggatga cttt                                     314

```

(2) INFORMATION ON SEQ ID NO. 37:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1839 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

gcggggcgagg gcggagcaac agagcggccg ggagtaaggc ggagtggagag gaggagcttg 60
atggaaagcgt gcgagaaggg gcgtaaactga ttgggaaacc agaggaaagg cgctgttttc 120
accgaattag aatcgcgagg aaatagagaa gagtttgttt gaagggtctcg cgagatcgag 180
tgagtacggc tcgccaaagt ggagcgctct cgcgatagac acagcaacta ttcagctggg 240
agggggcggg agagggtggg agcactctcg cgagatttga agggagcggc gagggcagag 300
ggaggagagg accggaagtc ctctatctca agcatccaat gctgaaacgg gcctgatttt 360
ctctaccgga agcccttttc cagagggtgg gaacacggcc cacctagcag gaagtccac 420
ctccttgagc tcgccacacc ttcccgaaat tttctgtca cctgtgttag gctcgtccc 480
ctttccgggt tttatcccg taccagaaaa ggatacatat agtgcctccc acccagctcc 540
actaaacggc ctcccgctct cctgtgttg tgcccgctgt gctgtgggga gggcccccga 600
cccgggggct cattcgagcg accctggacc acaatgccag catggaattt gcagaccttc 660
cagctctgtt tggggctacc ttgagccagg agggcctcca ggggttccct gtggaggctc 720
accagacaaa tgcctgcagc ccatttgccc caccaccccc agccccggtc aatgggtcag 780
tcctttattg gctgcttcga agattcgact gcaactttga cctcaaggtc ctaaatgccc 840
agaaggctgg atattgtgct gctgtagtac acaatgtgaa ttccaatgaa cttctgaaca 900
tggtgtggaa tagtgaggaa atccagcagc agatctggat ccgctctgta tttattgggg 960
agagaagctc cgagtacctg cgtgcctctc ttgtctacga gaaggggggt cgggtgtctc 1020
tggttcacga caataacctc ccttggggct attacctcat ccttttcaca gggattgtgg 1080
gactgctgtt tttggccatg ggagcagtaa tgatagctcg ttgtatccag caccggaaac 1140
ggctccagcg gaatcgactt accaaagagc aactgaaaca gattcctaca catgactatc 1200
agaagggaga ccagtatgat gtcgtgtcca ttgcctgga tgaatatgag gatggggaca 1260
agctgcggtt actccctgt gtcctatgctt accacagcgg ctgcgtggac cctggtctca 1320
ctcagacccg gaagacctgc ccattttgca agcagcctgt tcctcggggg cctggggagc 1380
aagaccaaga ggaagaaact caagggcaag aggaggggtg tgaaggggag ccaagggacc 1440

accctgcctc agaaaaggac ccacttttgg gttctagccc cactcttccc accctctttg 1500
gttcccttag ccagctctcc cttgtttttc ctgggccttc aacagatccc ccactgtccc 1560
ctccctcttc cctgttacc ctggtctaat aaccccccac acatacacct ctggtgacct 1620
atttgcacag accgtcgtct tcctccagtc cttctgaggg ataggggaca ttccatccca 1680
agcttctccc ttaccacacac ctatcctttt gaggggcttt ggggtggggg tggggcaagc 1740
agagggactg ggtcttcaat tcttgggcta ataaaaattg ttctttgttg actaaaaaaa 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1839

```



## (2) INFORMATION ON SEQ ID NO. 38:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1931 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

cagccgcgcgc ccatccctct ttgtgtgctt tggaaagccg cggagctggt ggtggctaca 60
gttgggtgttg ggggcttagg cgagggagct taccgggaag ttgcaggcgg gaggactctt 120
ccccatccag tcacctgaca ggtcacaaac atgtcagaca aaagtgaatt aaaggctgag 180
ttggaaacgta agaaagcagc actggcccaa atcagagagg aaaaagaagag aaaagaagaa 240
gaaaggaaaa aaaaagaaac agaccagaag aaggaaagctg ttgctcctgt gcaagaagaa 300
tcagatcttg aaaaaaaaag gagagaagct gaagcattgc ttcaaacgat ggggctaact 360
ccagaatccc ccattgtccc tctcctctatg tctccatcct ccaaatctgt gagcactcca 420
agtgaagctg gaagccaaga ctctggagat ggcgcctgtg gatctagacg aggcactatt 480
aaacttggaa tggctaaaaa caccgaagtc gactttccct ctcgagaaat tgtcacgtat 540
acaaagaaaa ctcagactcc agttatggct caacccaaag aaagatgaaga ggaagatgat 600
gatgtagtgg ctcttaaac accctattgaa cctgaagaag agaaaaactt aaagaaagt 660
gaggaaaaatg atagtaaaag tcccctctat gagctgactg aagaagaaaa gcaacaaatc 720
ttgcactctg aggaattttt aagtttcttt gaccatttcta caagaattgt agaaagagct 780
ctttctgagc agatttaacat ctcttttgac tatagtggga gagatttga agacaagaa 840
ggagagattc aagcaggtgc taaactgtca ttaaatcgac aattttttga cgaaactgtg 900
tcaaaagcata ggtgtgttag ttgtttggat tggtoactct agtatccgga gttactcgtg 960
gcttctcata acacaatga agatgccctt catgagcctg atggtgtggc cctgtgatgg 1020
aatatgaaat acaaaaaaac taccocagag tatgtgtttc actgccagtc agctgtgatg 1080
totgccacat ttgcaaaat tcatccaaat cttgtgtgtg gtggatcata ttcaaggcca 1140
attgtgtctt gggatcaacc tagcaataaa agaactccag tgcaaaagac tccactgtca 1200
gcagctgcac acacacaccc tgtatatgtg gtaaatgttg ttggaacaca aaatgctcac 1260
aatctgata gcatctctac tgatggaaaa atttgttcat ggagcttggg catgctttcc 1320
cacccacagg atagcatgga gttggttcat aaacagtcga agcagtagc ttgacatctt 1380
atgtccttcc ctgtttgaga ttgcaacaac tttgtgtgtg ggagtgaaag aggtctgtgt 1440
tacacagcat gccgcacatg cagcaaaagc ggaatcagtg agatgtttga ggggcatcaa 1500

ggaccaatca ctggcatcca ttgtcatgca gctgttggag cagtagactt ctcacatctt 1560
tttgtcactt catcgtttga ctggcacagta aagctttgga caactaagaa taacaagcct 1620
ttgtatctat ttgaagataa tgcagactat gtttatgat ttatgtgttc acctaccoc 1680
ccagccctgt ttgctcttgt ggtatggcat gggagattgt atttgtgaa tctcaataat 1740
gcacacagag taccaaactgc cagcatttct ttggagggtg atcctgcctc taactgtgt 1800
agatggaccc ttctgggaag gggaggttgt tgtggcggga ttctgaagga caagtttgt 1860
tattttggga ttttggggag agcagtttgt tgggtccccc aatgatggat tggcgacggt 1920
tggcccgacc c

```

1931

## (2) INFORMATION ON SEQ ID NO. 39:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 294 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

agttaccatt gccttttctg tctcgtgccg gttttggttt gctgaaaacta gtccaaaaca 60
ggaaatttaa cagacagcca cagccaaaga gtgcatgtg aattacaaga aatagagccc120
atttagggaa agatagaact agaaggctt ttcattataa ttccatgttg aacaattgag180
tcatagcctc ttatcttggg ggaaggacac aattcaaag ggccagtaag attttgtaaa240
acgtggcatc cataatttac tatggagcaa gtgccacat ctctaggaca ttaa      294

```

## (2) INFORMATION ON SEQ ID NO. 40:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 882 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

tttttttttc tcattaacaa agcagtcatt tccctttatt tttaaaattt tatgtacaca 60
tatgaatgat ctgtataatg tacattcaat atagaaagct ttatatattt gatagtgtat120
agaacatttc acaattacac tcattcttta cataacatct tgacatccat ttttaaattt180
ttttgcacaa gtcctctttc attcaatttg gtaaagccag ttatacatac taatgtgtac240
tgtgagcttt cagaagggtta atgattgagg atgccagtgga aggggtgcagg gacaaaacct300
aatagtcttg gatgggtggg ggaggatggc cagcgagact tgatgcagga gagggaaata360
ttctttctcg gggaaaaatg acttagccca atttttgttg actgtagctc aaccttacag420
tcacgtcagt tcaaaaaaaaa aattacaaaa actaggaaga aagttttgtc tttttgattc480
acagttttgt aaacagatat aaaggaacaa atgtgcttac atacaccaag aaaaaaaaaa540
ttcttgtgta ccactttatg ttgatccaca gattgtcttc ttataatgtg atacaattag600
gatcactgac tttttttcct aaaaatatat ttatagaaaa aggaataaca ctgtcatgaa660
accagagaaa aggcagtaag agtttgcttc aacgatcag ctggaggaat gtggactctg720
cactggcctt tcagcgctta ttgtctctcg tgaatatctc aagtctgata gccaaagtcg780
cctgcctcat ggtctacagg aggtggcagg ttagacatga ctgatgtaga tgtactcgcg840
taaggtagcc agcaactcca ggtcctgcct cagagagctc ca 882

```

## (2) INFORMATION ON SEQ ID NO. 43:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 934 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

ctcgccgccc acacagggag cagcgagcac gcgtttcccg caacccgata ccatcggaca 60
ggattttctcc gccccagccc aacggggagg gctagtgcga catagtgcatt tagatgaaag120

agctattgaa gctttaaaag aattcaatga agacgggtgca ttggcagttc ttcaacagtt180
taaagacagt gatctctctc atgttcagaa caaaagtgc tttttatgtg gagtcatgaa240
gacttcagg cagagagaaa aacaagggag caaagttaga gattctagta aaggaccaga300
tgaggcaaaa attaaggcac tcttggaaaag aacaggctac acacttgatg tgaccactgg360
acagaggaag tatggaggac cactccacaga ttccgtttat tcaggtcagc agccttcgt420
tggcactgag atatttgttg gaaagatccc aagagatcta tttgaggatg aacttgttcc480
attatttgag aaagctggac ctacatggga tcttcgtcta atgatggatc cactcactgg540
tctcaataga gggttatgctg ttgtcaccttt ttgtacaaaa gaagcagctc aggaggctgt600
taaacctgat aataatcatg aaattcgttc tggaaaaaat attggtgtct gcattctcag720
tgccacaat aggcctttttg tgggctctat tctaagagtg aaaaccaagg aacagattct720
tgacaagaaa aaaaacagag gcttttgctt tcttgatat gaagatcaca aacacgctgc840
ccaggcaagg cgtagggttaa ttgagtgga aagtcagggt ctggggggaa tgttggaact900
gtttgaattg ggggtgttcc gcttaggaag gtcc

```

934

## (2) INFORMATION ON SEQ ID NO. 44:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 231 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

ctcgtgcggg tcaattatga gttcctttat ttattgggtga gaaagattag caagtatgac 60
gtatgcaagg aatagaagtt atgtaccgag tgggtaaaagg ttgggggggat atggagatgg120
atgagaggga gctgtctggg aaggctttgc ttcaacttga tttagatgag gttgcgtga180
gaaatagggtg ttagaatga gaatgaggt catgacagcc tctacaaaa c

```

231

## (2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 240 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

cgatcacggtt ttcacatgat gctcacgctc agggcgcttc aattatccct cccacaaaag 60
ataggtggcg cgtgtttcag ggtctctcgt ctctctccta cagaaaaaaa aaagaaaaaa120
atgtcattag aagaggcgta acacgtcagt cgtccccag gtttgtgttt cctggagtgg180
ccgaaagaga tcagttctaa cctgctctgc aggaataacg gtcctgcctc cagacactct240

```

## (2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 228 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

agagcagatc agaggcaggg gaaaaagcac gcagagggag gagctgaaga gctgagaccc 60
ggagccaggg acagcttaat gaagacaaac tgaaggggaa actgagatgc ttagaaagcc120
cagctataca actctaccga gaaatacttc ccttagggaa tgtaaaaagt actactggag180
atggaagagc agaaaaacag ctatgggcag aaggccaagg ggtgatatg      228

```

## (2) INFORMATION ON SEQ ID NO. 48:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

aaaaaaaaa aaaaagagt taatctagga gataatgaat ggcctagtag tagataatat 60
atggccccc aaagctcttga cttctgtcct tggggaaagc cattttgtta accacactag 120
tgagatttat atgatgtcta atggagaaca gagaagatct tgttgcaaaa ggtgtattaa 180
atatattgtgc tgtttctgta tgagattgag aagcttttcc cactctccac cctattttcc 240
tataaggata tccagagaag ccaaaactgtt ctgtgggttt gggaatggtc atttccgggg 300
aaaatgcato tggatcgatg actaaacctg gcccttttct ctgggctgta gtgaagccgc 360
attttcacgc tggctggcag tgtgctgaga gccctgaatg ctctggcgcc tagtgccctt 420
ctgcccctgcc tgacgatgta tcgaaaagat gagagtgaag gagactttgt gcagcaggaa 480
acgggttaggt gaggtgtgtg gcagttgttg gaactcttga gagtattaca gagtgttaga 540
atcggtaaga actctgattt ggaacttcgt ttggtggaac tgtgtgccta tacctgcctg 600
tgtgtgtgca agtgtgcagg ttccctttgta tgtatgtgta cgtgtgggaa cctgtgtttg 660
tcataattttt cttcatttca caaaggcctt ttttgaagca gtggcagtat gcccttggtt 720
caagaacaca tgaattcttt ttaacaccag attagtgtgt taccccaaat gaacggttct 780
agccctctat taagaaataa agggaccata agcatttttg ctgcttatgg ctgtgtgtta 840
ctacttacaa gagtcttgaa aattatacag aactttgcct tcttttttta atgtcttcca 900
caatgttgtg actgattata accctgtttc cctccagaga agagctatgg ctcagggtatc 960
tgtgttgact ctggcattta gtggctttgt gaaggaaaga aaccattaaa tgacctgaca 1020
aaaactgact catgtcttta aagtgttgta agccactttt aggaatgtta ctctcggttg 1080
cttttgtcta attctaaatgg gcttaaaagcc aagaaaaacca tagtataaat ctttttgtgt 1140
taccctatgg ctagtgtttt aaatgggcag ttccgttgtg gataaagtat ccagtcactt 1200
caggtttccg tggaagggtt ttattggggg

```

## (2) INFORMATION ON SEQ ID NO. 50:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 231 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

gaggccggga gtggaacccc ctcttttgag aaggttgctt gactcagaga cacagaaacg 60
ggtccaggga tggggagaga tgtggagtga gggaaggttt gcatttgaga aaggaagtct 120
gagaacacac tgggacattg taacacattt gaaccatctt ctgatagaaa ggtgttggcc 180
tcctaataat gggaggtcag gcccaggtcc tcgggcatag ggagagggtc c 231

```

## (2) INFORMATION ON SEQ ID NO. 51:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1340 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

tttggcattca ttacaaattt catagaatta ctgtgaaggc ctttctagtt gagatgttgg 60
ggtattttggg attctaattg ttaaccccag aagaaggtaa tttagcttgt atttattttaa 120
aaccatttta gcttttttac tatatctggg agaattccag tgaatcatct aataaggrat 180
atttcagaat aatttttttt tccttcagaa taacttagaa tcagatgcta taagggtctcc 240
tagggagcgt gtgaaatttc cgtaaagata aatttgaatg ttgtaaccaa gtttatatta 300
aaccagagg ccattttccaa tatgattttt tgtttctttt taacttgcta agtccctaag 360
agattacatg ctagggtctg agtcatcttt attgtagata atgatggccc acacagtcac 420
cttcaactat ccacataagc taggcttttc gcttttgcca cggacagtggt gaccaagata 480
tttccagagt aaataaccca ccacaacctt ggtaattcct cttttcttct taagctccag 540

gaagcgaaag cagaaggact cttttcagac tgcctctctg agcctacatt gcagctttcc 600
aaaacaggca gctagcactg ggaaagccca tgtgggtgac ccatattttt ctgaggttct 660
tcttttccat ggtgttactt tattatcaga aagtataatc agaaaacagg tcttgccctt 720
agcagacaag aaccacacca gtttcttgta aaggtaacgg atacattggg attcaggagt 780
gacacagagg tccagcccca gaacttghtaa ggattttgtt tgaacctga gcagatgcct 840
ctccctgcc acccatcaca ctagttaggg ctggccatga attctatgcc agagtcactc 900
ctgcagtcgt ctagggatgg gccttcttat cccactctcg cacacatccc agtctagtct 960
ttgccttcac agagtctctc ttgacacccc tgacttaatg atagtgtctg ttttggagta 1020
gaattgatca ggtttaagtc atcctgctca ggttgggcat agtggctcat gccgtaatc 1080
tcagcacttt gggaaagcaa agtggggagg ttgcttgagc ccaggagttc caaacccatc 1140
tgggcacaag agggagaccc tgtctctacc aagaaaaaaa aaaaaaaa aagttaaaal 1200
aaaacaattg ctggacctgg tgggtgcacac tcagtaggct gaggtgaaag gattcctttal 1260
acatggggga ctgaagatgc agtgagccat gaatcagcaa ctgcacacca gtatgagagal 1320
aaaagtggaa ccttatcaca

```

1340



## (2) INFORMATION ON SEQ ID NO. 52:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 226 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

gccagatttc cggggttttg cgggccccgc gatgttttcc agaggttttc aagtgggaag 60
aggagagcga caaggtgaaa atgccccgtg ccggggcgctc cagcggagtc ctgccagctgl20
tccggcggtg ggggtggacgt ctgatttatg aaggtgccca tccacctatc tgaagtacctgl80
acttgtgagg actgacaact acagcatcag gtacaaagtt gttctt      226

```

## (2) INFORMATION ON SEQ ID NO. 53:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 611 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

gcagctgcag cggcagcagc ggcagcagag gcagcagcag tagccaccac tccgccgagg 60
cgccaacccc ggctcgccct cccaggcccc cgccgctgcc gcagtcattg ctgctgatgg120
ggcggagcaa cgctcgccct tgcgtgcagc atccactccc ggaaatgtca ctcccaccgcl80
cccaccgtac ttgcaagaaa gcagccccag agcggagtc caccctccata tacagccatt240
gccagtcag acgcccagtg tattccagta ataaactgcc gtgtgtgcc atcactaatc300
aatttgatg gcaagcttca ccagcatgtg gttaaagtca cagtttgcaa tgaagctacg360
ccaatcaaaa acccccacac aggcagaata tatgttagat gcccttgtaa ttgtcttctc420
atttgttaag acacatctcg gcgaatagga tgcacaagac ccaactgtag acggataatt480
aaccttggcc cagtaaatgt tatttctgaa ggaacaacca gctcagccgt cattgcccaa540
tcccaccag aagggtacaa gggctgtgtg ttggggcacg gttggggaac acattccctt600
tgggatggga c

```

611

## (2) INFORMATION ON SEQ ID NO. 54:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 689 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

gcgcagccgga cgcagggggc tggcgggaac gtgaagctcc gcgggtccgt atggggccgt 60
tggggcgccg gtactgtttg ctgttggggg accccctcat tccctgccgt gccgtccctg120
ctgcctcatg cgggcatcg gagttcacct gggtgcacc tcagcctgtg tggccgtcta180
taaggatggc cgggctgttg ttgttgcaa tgatgccgtg gaccagatta ctccagctgt240
tgttgcttac tcagaaaaatg aagagattgt tggattggca gcaaaaacaaa gtagaataag300
aaatatttca aatcacgtaa tgaaagtata gcagatccgt ggcagaagct ccagtgtacc360
acaagctcag aaatcacatg cggaaagtta atgtttagtc attgaaaaaa atgggaaatt420
acgatatgaa atagatactg gagaagaaac aaaaattgtt aaccagaag atgttgccag480
actgatattt agtaaaatga aagaaacggc acattctgta ttgggttcag atgcaaatga540
tgtagtattt actgtcccggt ttgatttttg agaaaagcaa aaaaatgctc ttggagaagc600
agctagagct gctggattta atgttttgcg attaatccac gaacgctctg cagctctctt660
tgcttatgga gttggacaag actccctta

```

689

## (2) INFORMATION ON SEQ ID NO. 55:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 560 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

agaaaatgga cgctgacatc aatgtcacaa aagcggatgt tgaaaaggcc cgacaacaag 60
ctcaaatacg tcaccaaattg gcagaggaca gcaaaqcaga ttactcatcc attctccagal20
aattcaacca tgagcagcat gaattattacc atactcacat ccccaacatc ttccagaaaa180
tacaagagag cggaggaaaag gaggatttgt agaattggag agtccatgaa gacatatgca240
gaggttgatc ggcagggtgat cccaatcatc gggaaagtgc tggatggaat agtaaaagca300
gccgaatcaa ttgatcagaa aaatgattca cagctggtaa tagaagctta taaatcaggg360
tttgagcctc ctggagacat tgaatttgag gattacactc agccaatgaa gcgcactgtg420
tcagataaca gcccttcaaa ttccagagga gaaggcaaac cagacctcaa atttggtggc480
aaatccaaag gaaagttatg gccgttcac ctttatgtc cttttaacg540
gggggccccat tcagcttcag                                     560

```

## (2) INFORMATION ON SEQ ID NO. 56:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 851 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

gaagaagagt aagaaggaca agaaggccaa agctgggtctg gagagcgggg ccgagcctgg 60
agatggggac agtgatacca ccagcaaaaag aggtagaatt ggtttctgag tagtgaaggc120
cacttgaagc tggaggagaa actaaagcct tattgagaaa acatgttata gatccttttg180
ttgctgagag agtggaaacat aggtcctaga cagggtgaa agttctggca catttttagct240
gctactttga gacctcggtg atgttacctg gtgtgggtcat cccatcttgt cctgttttaa300
ggatatgggt ggtgaaagat gaaagaggca gagtttatcc caatgaactc tctgtttgag360
ttggggaagc tcaccttcag acccagtaac tgtccgcagc tgtctgctag tggttgtctt420
aacatcgtag tctctagttg cattttttaa atccctctg tttaaaagg tgtgaaaaca480
aaaaacaaaa actaagtctg ctcaagtcaa tgctgtagaa ccctaaaataa gtggtagaag540
agtgtcaactg aattttgtct ctgaattcag tataactgag ttttgtccat gctgggtgct600
gggttatagg cctgatgggc ctggtagttt tccatcttgt tctggcctag aggtcagtc660
tttgcacttc ctcaaaagctt gtgtacagtg ctcaactaaa tccatctgac tacttgttcc720
tgtgccctct tgttttaggc ctgcgtttact tttaaaaaat gaaattgttc attgtcggga780
gaagaatggt gtaattttta cttattaaag tcaacttggt aagttttaa aaaaaaaaaa840
aaaaaaaaaa a                                     851

```

- (2) INFORMATION ON SEQ ID NO. 57:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1354 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

cttaccaca gctttctgc taagtctgt ttttggata tttatgactt ggttcattctt 60
attttttcct gatttagcag gagccccctt ctatttcagt ttcattttca gcatagtagc 120
ctttctatac tttttctata agacttgggc aactgatcca ggcttctacta aggtctctga 180
agaagaaaag aaagtgaata tcataccct tgcagaaact ggctctctgg acttcagaac 240
attttgtaca tcagtgttta taaggaaaggc attaaggcca ctccactgcc atgtatgcaa 300
ctgctgtgtg gctcgatatg atcaaacctg cctgtggact ggacgggtgca taggttttgg 360
caaccatcac tattacatat tcttcttgtt tttcctttcc atggtatgtg gctggattat 420
atatggatct ttcattctatt tgtccagcca ttgtgccaca acattcaaag aagatggatt 480
atggacttac ctcaatcaga ttgtggcctg ttcctcttgg gttttatata tcttgatgct 540
agcaactttc cattttctcat ggtcaacatt tttattatta aatcaactct ttcagattgc 600
ctttctgggc ctgacctccc atgagagaaat cagcctgcag aagcagagca agcatatgaa 660
acagacgttg tccctcagga agacaccata caatcttggg ttcatgcaga acctggcaga 720
tttctttcag tgtggctgct ttggccttggg gaagccctgt tgggtagatt ggacatcaca 780
gtacaccatg gtcctttcac cagccagggg gaaggttctt cgctcagtat gaagaaaaagc 840
aaccacaaac tctcaatctg atttgttttt gtttatgtcg atgcccgtga gtttgaagat 900
gaagtaaaag tttagaattc acctaaagtc aaaggaaaaa acgtgggtttt taaagccatt 960
aggtaaaaaa agttctcaat aaaggcatta caatttttta gggttagaaa gatggacttt1020
tttgataaat cttggcgacac atctaaaaaa aaaaccatat ttttcacaag aaaatgcaag1080
ttactttttt tggaaaataat actcactgat tatggataaa atggaatatt ttcagatact1140
atatggctg tttcaaaaata gtactattct ttaaacctgt aatttttctg aagttatttg1200
tctttgttgt atctataaat atgtaaaaaa tatttaaaata gatgtacctg ttttgccttt1260
acacttaata aaaaaatttt ttttgtaaaa ggaaaaaaa aagaagagga aaaagaagag1320
aaaggagagg ggaagaaaga ggagaaggca agga 1354

```

## (2) INFORMATION ON SEQ ID NO. 58:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 268 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

cgtgatctct cctcagtaaa accaaggtgc atttttctgg acccacctat cttgggggtg 60
attaggagta gagggttgta aatacttaaa atttttttcc ttctgatat aattattgat120
ctccttctag aagtctctgtc gtctttgctg gagaattttt attttaagcat cctttttagt180
aagaatctct aatgtcccttt ttctatccag atctacactt gatgaatcct aaagctattt240
ctacacagtt cctttattca gttttccc

```

268

## (2) INFORMATION ON SEQ ID NO. 59:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 752 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

tgacaaaaga aatggaataa ttccaaaaaa gttaagtcct gagaagacaa ccctgaaatc 60
tattttgaaa agaaaaggca ccagtgatat cagtgatgaa tctgatgaca ttgaaatttc120
ttccaaagtca agagtaagaa agagagctag ttcatgtagg tttaagagaa taaaagaaac180
caaaaaagaa cttcacaatt ctcccaaaac aatgaacaaa acaaaccaaq tgtatgcagc240
aaatgaggat cataactctc agtttatgta tgattattca tcttcagatg agagtttatc300
cgtcagccac ttcagtttct ctaaacagag ccacagacca agaactataa gagacagaaac360
tagtttttct tcaaaattgc ctagccataa taagaaaaat agcactttta ttccaagaaa420
accaatgaaa tgttcaaatg aggaaagtgt ttaatcaaga gcagtcgtat gaatcaattgg480
ataaaatttt agatggcgtt caggaaagtgg cttatatcca ctcaaacag aatgtaattg540
gatcgagcaa agctgaaaat cacatgagcc gatgggcagc acatgacgta tttgagttga600
agcagttttc acagctgaca gctaacatag ctgttttcag ttctaagaca tataaagaaa660
aagtggatgc agatacattg ccacacacaa agaaaaggcca gcaaccgagt gaaggcagca720
tttcacttcc tctttacatt tcaaatcctg ta

```

(2) INFORMATION ON SEQ ID NO. 60:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 1389 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

gaactccaag ttagtggatt gcagaatgga aacttggctt ttgcggcact gggtagattt 60
tagttttgtg gtgtcttgct ggggggtggt gatgattgtc tcagcactca cgcactgcac 120
aagatggcag caggatcacg cactgcacaa gatggcagct cctctgcagc ttccctcctc 180
gcctccctcc ttgcaccccc acaggttttg cttgggtttt ttgtcatcag taacctactg 240
cctgagatca tgacctctta aaagatgaga ccttcggaag ggttgattgt atgcgtcagt 300
gagcctctta tcaccttctg gaacaaagt ccttgaaatc tcttgatgag attaaggagt 360
ttagtgttac taagaaaatc tgctttgggc cgcagcagtg ctgggtgttc tcagacctga 420
ctgaggaagt tagctgcggg ctgcccctgt gctggtgtgt tcagagagaa tccagagaa 480
tggtcagatg ccccccttgg gctcctttct aatcttaac agctctttaa atagctgcc 540
atctcctgtg attgcacaac caagcacttt gacatttgca ccttaggaga ggcagatgtt 600
aaaaatggaat ccaaaagacca cctaggggcg ggttgggtgg gagatgggag ggccaactgc 660
gagctgtctc acttctcagc tctccccctg cctgcagccc tgggccagac aaggccagaa 720
ggtttcaggg gcatttgaca tccccctctg gttctcacca ggaaaaacac caaagctttg 780
gaggaacacg gccctgcccc tggctcctta aatgcccggt ctcttcttaa actgatatcc 840
agccagcaat gcctaagact ttgttaagat catttctact gcttttcttt ctgcttcaaa 900
cacacagttc gtctctgagc aaagtaaaat aatggaata agagttaaatt gggtaaggag 960
atatccaaag ctaccagtc ccttgaccca gcacagttgg ccgaccctgt tcaactccctg 1020
gctgtcgtgt cttctctgtg ctcactgaag ggtgagccag gccagtgtct cccacgcccc 1080
tgggcctggt cactacacag tggaaaaacg acaagcgccc ccttccccaa atcccaagag 1140
tgtcttctgt cttgggtggg gctcatcgca atgttctgaa ggctccaggg ccactttgtt 1200
tgtaaagtat attcgggccc caaaatacca tagtagctgc ttgataaaat tctaaaaaat 1260
tctggttctc tattatgtaa acactattac agtcaccagt ggtgtaagac tcttgagtct 1320
ggttctcata tcagagtcat catttttctt cctgtggaat aaaatgcctt gggactcccc 1380
caaaaaaaaa

```

## (2) INFORMATION ON SEQ ID NO. 61:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 726 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

cgtatctgtc cggagcggaag caggaagcgg gagcggttag gccacgcctg cggcgctgct 60
ggttgaggct gtgtgggtgg gggacgggccc gaggcgatgg cggagaagtt tgaccacctal20
gaggagcacc tggagaagtt cgtggagaaac attcggcagc tcggcatcat cgtcagtgac180
ttccagccca gcagccaggc cgggctcaac caaaagctga attttattgt tactggtctta240
caggaatttg acaagtgcag acagcagctt catgatatta ctgtaccgtt agaagttttt300
gaatatatag atcaaggtgc aaatccccag ctctacacca aagagtgccct ggagagggct360
ctagctaaaa atgagcaagt taaaggcaag atcgacacca tgaagaaatt taaaagcctg420
ttgattcaag aactttctaa agtattttcc gaagacatgg ctaagtatcg aagcatccgg480
ggggaggatc accgccttc ttaaacagct caccctccct gtgtgaagat cccctgggac540
tgcgatgcgg cgtgaggctg ggactgcgag tgctgacgcc accttccctg cgtggtggga600
ctgggcccctg gacacacccc tcagccccctc tgcctcatt gtttgccctc atgggaccga660
ggggctggag gagagggcga gtgtgcccac gggttcaaga ggttggtttg ggtgaaatgg720
gtttgt
726

```

## (2) INFORMATION ON SEQ ID NO. 62:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 681 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

ggctgagaaa aatgggggga gacataaac ccacgaatga aaatacagat ttaagagaag 60
gaaccagttaa agtaggagac agatgtgaag gaaatggaaa tgaggcgaaga ggacattgga120
agagagaaagt ttgtgtttaa gtagccaggt ctggagcatt agtvtgaggg agttcaggta180
ggctggggcct gtgcctcttag gtaggggaaa gggaggctgg gttagccaggg ctgggtgctta240
aaacccctcga ggccatgagc tcattggctg cctttgtagc atcctgtctt cctctgtgct300
gctgtgtgtg atctcatctc acctggatbc aaagggttaa gtgggcatgg gtcttggggc360
tgacacccca caaggatgac ctgtggactg ccactcggatg ctgaacaggg agatgaaagg420
aggttcctctt acctatcccc tctgccaaac cccagtagtg ccactgttct gactttgttt480
ccagaatata cagaaatcca aaggggctgt tgcgtgaacag tctgcaggac cagtgcagcg540
acctacctgt tgtcccaagg catcaaaagg aggcctcaac gctcatgctt ctctaataca600
gccctaccac gacagacaga aaaggaaagg gttagaggaga aggttgaaac tgtggaggtta660
gacctctgctt cacttctgaa g
681

```

## (2) INFORMATION ON SEQ ID NO. 63:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1116 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

gggccacact gaggcagattc ttgtgtagaa ttttcaactt gagactaaca caagtatttc 60
cttttctgtt cagttctcca aatgacaaga agtctttttg ctcaattgaa ggggaatgga 120
atgggtgtat gtatgcaaaa tatgcaacag gggaaaatac agtcttttga gataccaaga 180
agttgcttat aatcaagaag aaagtgaaga agttggaaga tcagaaacag tatgaatccc 240
gcagcctttg gaaggatgtc actttcaact taaaaatcag agacattgat gcagcaactg 300
aagcaaaagca caggcttgaa gaaagacaaa gagcagaagc ccgagaaaag aaggagaagg 360
aaattcagtg ggagacaagg ttatttcatt aagatggaga atgctgggtt tatgatgaac 420
cattactgaa acgtctttgt gctgccaagc attaggttgg aagatgcaaa gttttacct 480
gatgatcagg gcagtaggca taattcagca acaaaacaatc ttcttttggg agaaacctgt 540
tcattccaat cttctaatta cagtgggttc tatctcagg atactggact ttctgacgca 600
gatgaacaat taaggggaaa agcttccctt ttccctctgt ggcagttaac attttgactt 660
cagtcctgag aaaaacttca ggttttgaaa atcagatgat gtcttctcct ttcccaaaaca 720
ccacacgttg aaagcattta taaatccaag tctgaaactc tgcgctctag tactgtgtgt 780
aagatacacac actgttttct tagttcatat aatctcgggg acacacatac gtatacacac 840
acatacatat atataaatat acctgatgcc agattttttt cataaatatt ctgcctactg 900
taaatatggg ttctctcag tggttttaga aaattagcgc aatgtattaa aatcaagtgt 960
taggaaaattt ctatggctta cctacaataa cttttatttt ggaattgaac tattattaaa 1020
ttgtatctaa tcttgggaata cagtttaatt aattattcct agtgcttaag gcttcataaa 1080
gtaatttttc caaccttttt tttaaaaaaa aaaaaa
                                     1116

```

## (2) INFORMATION ON SEQ ID NO. 65:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 806 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```
tccaagggct ctttagtctt tcttaagccc cacagtaact tcccgtagtc ctgagggttg 60
ggacctctcg gggttcttac ctccctcccc cattgctgag acagtctgag aagaggcttal20
ggaatttgtc tgtgggagtt tattcatctg tctctcttat ttacctctcc caaaccaggga180
tttccacttc tcaaacctgc tgtgatctca caactggagg gaggaagtga gctgggggggc240
tcattctccac tggctgcagg aacaggcctc cagggtctcc agactgatat tcagactgac300
aatgatttga caaaggaaat gtatgaagga aaagagaatg tatcatttga acttcaaaga360
gacttttccc aggaaacaga cttttcagaa gcctctcttc tagagaaaca acaggaagatc420
cactcagcag gaaatatataa gaaggagaag agcaacacca ttgatggaac agtgaagat480
gagacaaacc ccgtggagga gtgttttttt agtcaaaagt caaactcata tcagtgtcat540
accatcaact gagagcagcc ctctgggtgt acaggattgg ggaatccat cagctttgat600
acaaaactcg tgaagcatga aataattaat tctgaggaaa gacctttcaa atgtgaagaa660
ttagttagagc cctttagggtg tgactctcaa cttattcaac catcaagaga acaacactga720
ggaaaagcct tatcagtggt cggagtgtgg caaagcttcc agcattaatg agaaattaat800
ttggcatcag agacttcaca gtggggg
```

(2) INFORMATION ON SEQ ID NO. 67:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 226 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

gcgggataccgg cgttctctcac tgatcttttc caagggtgta cagagatggc gccgggtttt 60  
cggaaggcgg gtaagtcccg gacgcgggaa cacagagagc gaagcgaagt actaccgtaa120  
aaaaacaagtg acctcaaaag ttgttcggaag aagggtgtgc aaaaaatacc agtgagttct180  
atacacaaat gactcggggt aaactcgaag tqgggtatca aattat 226

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2042 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

gcagccgtcg ccttcggagc gaaggggtacc agcccggcag aagctcggag ctctcggggg 60
atcgaggagg cagggccgcg ggcgcacggg cgagcgggcc gggagccgga cgcggcgagg 120
agccggcgag agcggcgcgg cgggctccag gcgagggcgt cgacgcctct gaaaactctg 180
gcgcgcgcgc gcgccactgc gcccgagcgc atgaagatgg tcgcgcctgt gacgcggctc 240
tactccaaca gctgctgctt gtgctgccat gtccgcacgc gccacctcct gctcggcgct 300
tggtatctga tcatcaatgc tgtggtactg ttgattttat tgagtgccct ggctgatccg 360
gatcagtgata acttttcaag ttctgaactg ggaggtgact ttgagttcat ggatgatgcc 420
aacatgtgca ttgccattgc gattttctct ctcatgatcc tgatatgtgc tatggctact 480
tacggagcgt acaagcaacg cgcagctgga tcatccatt ctctgtttac cagatctttg 540
actttgccct gaacatgttg gttgcaatca ctgtgcttat ttatccaaac tccattcagg 600
aatacatacg gcaactgcct cctaattttc cctacagaga tgatgtcatg tcaagtgaac 660
ctacctgttt ggtccttatt attcttctgt ttattagcat tatcttgact ttttaaggggt 720
acttgattag ctgtgttttg aactgctacc gatcacataa tggtaggaac tctctgtatg 780
tctcgtttta tgttaccagc aatgacacta cgggtgctgct acccccgtat gatgatgcca 840
ctgtgaatgg tgctgccaaq gagccaccgc cacttaactg gtctgctcaa gccttcaaqt 900
gggcgagtg gggcgagcag ctgacttttg cagacatctg agcaatagtt ctgttatttc 960
acttttgcga tgagcctctc tgagctttgt ttgttgcgtgaa atgctacttt ttaaaattta 1020
gatgttata tgaactctgt agttttccac atatgtcttg ctagaacact gtgatagatt 1080
aactgtagaa ttcttctctg acgattgggg atataacggg ctccactaac ctccctagg 1140
cattgaaact tccccaaaat ctgattggac tagaagtctg cttttgtacc tgcggggccc 1200
caaatgtgg catttttctc tctgttccct ctcttttgaa aatgtaaaat aaaacaaaaa 1260
atagacaaat ttcttctcag ccattccagc atagagaaca aaacctatg gaaacagaaa 1320
tgtcaattgt gtaattcatg ttctaattag gtaaatagaa gtcccttatg atgtgtttac 1380
agaatttccc ccacaacatc ctttatgact gaagttcaat gacagtttgt gttcgttggt 1440
aaaggatttt ctccatggcc tgaattaaga ccattagaaa gcaccaggcc gtcgggagcag 1500
tgaccatctg ctgactgttc ttgtggatct tgtgtccagg gacatggggg gacatgcctc 1560

gtatgtgtta gagggtggaa tggatgtgtt tggcgctgca tgggatctgg tgccctcttt 1620
ctctcggatt cacatcccca cccagggccc gcttttacta agtgtttctg cctagattgg 1680
ttcaaggagg tcatccaact gactttatca agtggaaatt ggatataatt gatatacttc 1740
tgcttaacaa catggaaaag ggttttcttt tccctgcagg ctacatctca ctgcttttga 1800
cttccaagta tgtctagtca ctttttaaaa ttgtaaacatt ttcagaaaaa tgaggattgc 1860
cttcttgtta tgcccttttt accttgacta cctgaattgc aagggatttt tatatttca 1920
ctgtttcaaa agtcagcaac tctcctgttg gttcattatt gaattgtctg taaattaaqt 1980
tagttgcaat taaaacaagg tttgccacca tccaaaaaaa aaaaaaaaaa aaatgggtgg 2040
cg
2042

```

## (2) INFORMATION ON SEQ ID NO. 72:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2980 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

|             |            |            |             |             |             |      |
|-------------|------------|------------|-------------|-------------|-------------|------|
| cagagtgta   | gcgcagaa   | cctcctgtg  | ccccagcct   | agagagctc   | cattctcaac  | 60   |
| attgagctga  | aagggctcaa | gcccaaaag  | gcacaaagc   | ccccagctc   | cattcttcag  | 120  |
| ctccctcgtg  | gcgcagtgat | cctgttaa   | ctgtggaggt  | cagctctgagc | taccaagact  | 180  |
| ctccctagac  | aaaggtggag | tcccccaac  | tgcccaagac  | caaatccact  | actcaacctc  | 240  |
| ctgaggtgtg  | gatggggcaa | cagagcaaa  | actgagcaac  | ctgatgcatt  | cagcctgctg  | 300  |
| tgacagagtg  | ccatttactg | ccctgatgtt | cagagagaaa  | cgcacaaaac  | gattgtcccat | 360  |
| gagatttggg  | gcagagatgt | ccaagacgtg | ctgttatgtc  | gttttctctg  | gtgtatgaat  | 420  |
| caggaaagtg  | tgtgtgtotg | gaggccaatt | ctgtgttaatt | cttttcccat  | gtgttgaagt  | 480  |
| ttttagaaatg | cttaaccttc | ggacagtgc  | ctgtcattta  | tcagagacct  | attgtgaagt  | 540  |
| ttctctcttc  | ggcttctgtt | ttctctggac | agttttagat  | tggggagcct  | attctccatg  | 600  |
| gcgcacaaaa  | atgatgttca | gtgttactt  | taactaacac  | caatgtatc   | tggtgtctgg  | 660  |
| ggggacagcc  | ataagcaaga | catgcccagg | gtttgcctgt  | gctccagatc  | tactccctgt  | 720  |
| aggagtgtcc  | ggatcacaga | caacgttagt | accagggttg  | tgaaatctag  | tacacctcgt  | 780  |
| caagggctca  | cttcagactg | aagcagcaat | cttgcacata  | cagcagcaac  | ccaggagctc  | 840  |
| tggtttttgt  | ggggggcaga | tcagaagaga | gaggccccgt  | tgatccctgg  | gctgttgtgt  | 900  |
| ccacaactct  | tcocattcaa | ggatgtttat | ggcctctctt  | tgatcctctc  | gtgagacaaa  | 960  |
| tacagaaatg  | accocattcc | tgccaccagt | aaactcagag  | gtgatgtggg  | agactgacac  | 1020 |
| aggaaaaatg  | actctaatac | gcagacatgt | gatattgtgt  | aagaagaatg  | tgaggggaggt | 1080 |
| agagatgaat  | tttccctgga | gggatcctag | aaagcattgt  | ctgatgtcca  | ttcccatatg  | 1140 |
| ctccactttta | aaacaatagt | gtgtgtgaag | aacctttgtc  | tgagggtagt  | tcacagctgt  | 1200 |
| aaataacttg  | aaattttcc  | agagttctta | aactctcttc  | ttccccaca   | gatcacacat  | 1260 |
| caagctcaca  | aataggagta | gcaattctag | gtgttagggg  | tgtgtacgga  | accctctggt  | 1320 |
|             |            |            |             |             |             |      |
| gtctgcata   | actccagaat | taccccagga | ccattgtccc  | aaagtctaga  | gtcttttcag  | 1380 |
| gtaggcaaaa  | tttgttttca | attgcctgtg | ctcagctgtg  | gtcacaaata  | cccatcttag  | 1440 |
| gatcccatca  | gcttcccatc | ccccacagca | cagccacagt  | accctcactt  | ttctcccttt  | 1500 |
| gttcttttca  | attcgtttct | gcagaaagaa | actgcacata  | attcatccac  | actcaagttg  | 1560 |
| aaatgatgtg  | taataggaa  | gagttacact | ttccacacga  | catttgtttg  | taagtatgac  | 1620 |
| agacagagtg  | cttaatccca | aggaaaaagc | ttatggacat  | ggaggggggg  | agctttctg   | 1680 |
| gtagaagagtg | acttccctga | tttccctaaa | accocagtaag | agtaagaact  | gttgttttgg  | 1740 |
| aaggtctgct  | ccacactcca | agagcagata | tttttttttt  | gtgtgtgtgt  | ttgttaacgt  | 1800 |
| ctctgaggga  | atatagtaaa | aatgcataat | cagctgcaat  | ttgcacggga  | gcaatttccac | 1860 |
| catgtgtgac  | tgatatggta | aatgtgtttc | ctgtgttttt  | gatcacaacc  | ataataacal  | 1920 |
| ctatccttca  | tcatagtttt | ttcaggggtg | cttctgtatt  | agtagggaat  | tttgaacac   | 1980 |
| tttttaaaaa  | cagctcagaa | ataaaaacaa | ttgtttaaag  | cacatttgca  | tcagtagcca  | 2040 |
| gctcacgcga  | tttgtatata | tcocaaaaat | cattgtatg   | tcocaaactt  | ggcgtctttt  | 2100 |
| aataaaatct  | ttgtgtaaaa | tttgtatcac | gtgcctcttc  | tatgtatgat  | gaacacagaa  | 2160 |
| acagagattc  | cccaattgtc | tttgtctctc | agacatttat  | taatatagaag | tacctatttt  | 2220 |
| tatgctgaaa  | ttgtttatca | tttgttatgt | tcagcaagtgc | actcaactgt  | cgcgatgctt  | 2280 |
| tgcaacacat  | tttgtatata | tagccatgct | tcgggtgtaa  | ggcagccccg  | aaactcctta  | 2340 |
| tcotttttgc  | ctctctcggg | atcagttaaa | gaaaaaataa  | ataatgtgtc  | taagaaggtg  | 2400 |
| gactgtgaat  | ttgtataatt | aatcttgtat | agacaaatga  | ctcactctta  | atagaaaaat  | 2460 |
| tttttttaaaa | atttgaatgt | aaaggggtta | aggaggttat  | gaagtttttt  | tgacttttaz  | 2520 |
| taaaatgata  | ggaattccaa | atgcactcac | tacagattct  | tagcacaata  | atgacattct  | 2580 |
| taaaagtgtt  | aaatttcaga | taagtattct | attggggagg  | aaaggttaact | ctgatctcag  | 2640 |
| ttacagtttt  | ttctttccct | tttaattttt | tttttgggtt  | ttcttggttt  | tgcaagtcac  | 2700 |
| ttctctgcga  | ctgtgattaa | ctctcatatg | tagaataggt  | tactacaata  | agggttatct  | 2760 |
| cttgagaagaa | aaataacatg | catatatatt | aacaaattaa  | tttaagatag  | tgccatttaa  | 2820 |
| attcacacat  | gagagcaatg | cctatgcaga | catagatttt  | tcctgtctat  | ttttttctct  | 2880 |
| cattgcagtg  | gactgatttg | ataaagatag | grgttgtaat  | actacatttg  | ctgtacatat  | 2940 |
| tttttaataa  | actttattca | gaattcgtgt | gcgaataaaa  |             |             | 2990 |

## (2) INFORMATION ON SEQ ID NO. 73:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 227 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

cagcattgct ccacggcaca gcataaggat agatcccaag tccacagggt ccattttgca 60
gggtcatattc tgatcctagg aaatgtcctt ttcccatagt tgtcctatgc ctttgggggtt120
tagtctatcc caggggtaac tgtggagaaa tcattgggtt gagagtcaag agagcattgg180
ttttggagct ttaatccctt tctggttgaa ataagggtgt caacttg                227

```

## (2) INFORMATION ON SEQ ID NO. 75:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 773 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```

cggaagtgtta aaggtttctcg cctctctctcg gccaggcgga acctctctgc tggggcccggt 60
ggcgcgcaaaa gaacttttctt ttctccgccc gaacgggtgc cgcggccaac tgcctcgcccl294
gcctggcagc ctaaccctccc ttctcttctt ctctctctcg gcttcgcgcg gccctcgctcl180
cctctcgccc ggcggcatcc gcttgctgct gccaccgctt cctcatcttc tgcccggcca240
accggcctgc cccgctgcag tgatgtgcga caaggagttc atgtgggccc tgaaaaacgg300
agacttgat gaggtgaaag actatgtggc caaggagaa gatgtcaacc ggacactaga360
agggtggaag aaacctcttc attatgcagc agattgtggg cagcttgaaa tccttggaatt420
tctgctgctg aaaggagcag atattaatgc tcagataaaa catcatatta ctctcttct480
gtctgctgct tatgagggtc atgtttctcg tgtgaaattg ctctctgcaa aggtgtctga540
taagactgtg aaaggccccc atggaactgc cgcctttgaa gccactgaca accaggcaat600
caaaagctct ctccagtgat ggaatgagtg actgataact ccggaagaat gactctctg660
tggcctcaca ctgctgcctg tctgtctgtc actctctatc tgcacagctc ttcagctaaa720
tacttttaaga ggggtgaggg gagagagaaa ttcataacaa atccgactac cag 773

```

## (2) INFORMATION ON SEQ ID NO. 77:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 870 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

```

gacccggcgt ggctactagg agaaggacgt acggctctgc tagtagagga atatgtcag 60
tttctctagg gcgccccagc aatggggccc ttttgctaga atatggtatc tcttagatgg120
gaaaactgcag ccacctggca aactgtctgc tatggcatct ataagacttc agggattaca180
taaacctgtg taccatgcac tgagtgaact tggggatcat gttgttataa tgaacacaag240
acacattgca ttttctggaa acaaatggga acaaaaagta tactcttcgc atactggcta300
cccagggtgga tttagacaaq taacagctgc tcagcttcac ctgagggatc cagtggcaat360
tgtaaaaacta gctatttatg gcatgctgcc aaaaaacctt cacagaagaa caatgatgga420
aagggttgcat ctttttccag atgagtatat tccagaagat attcttaaga atttagtaga480
ggagctttctt caaccacgaa aaataactaa acgtctagat gagtacacac aagaagaaat540
agacgccttc ccaagattgt ggaactccacc tgaagattat cggctataag agaataagaa600
ttgcagaaaa taacagtgaa gtgattgaaa ctctctctgc atgagtttct ctaacctaca660
ggatggagta aaacaactgc tacagttcag cactgttttt atgtgccgaa tcactgtgg720
gaaaggctga gaaggtgtag tccctcaata ggaatttgta attaaaaat aattttatag780
aacatttttt atgtaactct atttgaatgt tatagttgat aataataaaa tcacttact840
ggttgactaa aaaaaaaaaa aaagtgcagc 870

```

## (2) INFORMATION ON SEQ ID NO. 78:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 237 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

ttgtgatcgg ctatccttcc cggatcaaca gcgagcccg cccggtcacc tacaaccggc 60  
 ccgggaacaa cgtgaaactg aactgcattg ctatggggat ttccaaagct gacatcacgt120  
 gggagttaac ggataagtcg catctgaagg caggggttca ggctcgtctg tatggaaacal80  
 gatttcttca accccaggga tcaatgacco attcagcatg ccacaaagag gggtggc 237

## (2) INFORMATION ON SEQ ID NO. 79:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 439 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```

gtttgggaag ttgagatttg gagcgaataa gtagggatct ggcaagagga tcctctacct 60
cagtcattag gatttcttaa taaaaaagag attgtatttt tgagtgggtt attaaagattal20
ttaaaattag cccttccttt gaaatatgac atcagctttg ctgttctaaa tttaaaattal80
gttgcttcat cagtagcaca cttccagttt ctataccaag ccagtcctct cagttttccc240
cttaggatgg gacaagtctg ttcagggggt cattctgtaa gggtcagcag ggggtttggg300
agaggattta aggggaaata cagtgggggc agaatgggtt cgggggtaaa ggtaggggac360
aagggagggg gggcgaaagg aggggtggaa ggatgggggc cttacctaga tcgggggatg420
ccgggggggc aaggcaagg                                     439

```

## (2) INFORMATION ON SEQ ID NO. 80:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 2483 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
- (A) ORGANISM: HUMAN
  - (C) ORGAN:

- (vii) OTHER ORIGIN:
- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

gcaaaagtct tcaaaactatt gagaagaagc catagactga gtgcaggcac cagtgcgctc 60
ttattactgt gtcaattaaa tgaatgtatt tgaatgtttg gatacttacc tctgaatgta 120
tttttagtaa taacttcaag tgcaaatatg gccatgcata atttctttgg tctcatgttt 180
ttcccccttc ttcttttagg ctttgtcttc tgagtctata gaaaaacttc cagtttttaa 240
caagtcagcc ttcaaacatt atcagatgag ctctgaggct gatgactggg gtatcccaag 300
cagggaaoca aagaacctgg caaaagaagt ggccatgtga agagggacac tcaggacact 360
ttacgggatac aaagtgggtc tacaccaagt ctgcttctcg aatgtttgtg tgtgaacctt 420
tgtttccctc aaaaacaaag acagcaacga aaactcctta atcagaacac tgatccaatg 480
aggaatggag cttgtttctg tgacccagga gaacttagtg caagactaca ggagttaaca 540
gatggccagc tctctatttt ttaattgtaga ataactcctg agtttatatc aaatcctgaa 600
gaaataagcc tcagttttcc atctgttttt gataagaata agaaagggag tgagtgtgaa 660
gatggtgtgt agcagtttca ctaagactga tatttttagc ctctttgtta catcaaaaga 720
tattgtgtgc agaataccag cattttctcg ccactgcaag gattaaactc tagttttcac 780
tatgtgggtc caaatatatg tcaatgtaca ttttgaacat atttatgtgc tatggaaaga 840
aatgtcgttg actaaaataa ggtttactct gaaagaggag gaattttatt caaagcattc 900
aaacattttt ttcaagtgtt tcaaaattca aagcatttga ttcaaaagtg cagtgaaggc 960
atcaacttat gtaaaaactc agaaaggaag ctctctctgt aaaaaacacag ctcttttatt 1020
atcgtgcttt tcttgttcac tttaacacac aagtaaacac ttattgtcag gtgcctatgc 1080
tttagtgaat tgttagatgt gcactgaact cgggatgttg gggattggag agagagaatt 1140
gocaaagtta cagcaaaaaa atctcttaact ttgctttgtt tataaaaaaa ttagttagatt 1200
ggaaaaacta gtgttaggga aagaatacac atgttcagag cctaatttcag taggaaagggc 1260
ttttctctac cctgaaatga aggtaatcca aaggcatcca ttttctaggc tttaaaagata 1320
tatttttgat atatttaagt atatttctca cactccagca ttaatatgtc tgtttaaaaa 1380
ttactaattc tcaaatggct caagaacatt agaatttaag taccttttag gtaattattt 1440
ttaagcaaat agcctggagc taagagattc tcatgccagc atgctttcat ttgtcagttg 1500
tttgtactga gagataatga atgacacctg aaatgcataa ggtatttttg ggagagttaa 1560
ggtataattt gaaggttggc agaccagttg ggcgtgattac tcttagagaa gaagaatgg 1620
aaaaatgaaa gaaggcagga aggaagaaaa ggatatagga agagagggga gcagaaggca 1680
ggcatttttc tattttcccc acaaatattt tcaaaaaaaa tctgtatttt ctgggatatt 1740
tcattggcaa gaggaagaac tgggtgtttt aaagcagtat ggattcttta aatgcctctc 1800
cctgtacaaa gatagtaggc tttagataaa taaactcaac cgtgtcaatt aacattttaa 1860
ctggcatata gaaaaaaagg aggatttttc tgcattgtaa aataatcagt atggtttata 1920
tgttgtaatg gacatttgtg tgaattttca tgggtggccta gtgtgttggt gcttctggta 1980
tttgttaatg aagctcaact atttttttgt ggatttcaat ttttatcttc agaaagctca 2040
gacagtgaac ttctttaatg gtgggagttc agctcatgca tttctgatta tacaaaaaac 2100
tttgcagtag gttattttgc atttcagttt ttaactgaaa tcttagctaa acatttttac 2160
atgtaaatca ttgtatttac caaagattta aatcagttga ttaatttaatt aactcaaaaa 2220
ctgtgaacta cttttaaaaa actagaaaaa agaaatgtta gtatctcaat tacaccaact 2280
gtgcaaatga actttgataa aatagaaaaa atctacattg gcoctttgtga aatctgggga 2340
agagctttag gattctagta gatggatact gaatactcag gcccaactaa tttattaatg 2400
tatacatgtg gttttgtctt ttatgtctag tacagagaaa tgtgataatt ttttataata 2460
aatatttttt atgatgataa aag

```

2483

## (2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 353 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

gggtggtgggg gggggggtgt tgggccaaaa gacttcggta tctgacaaca gcatcatcta 60
cctcagtcac tagggtttct taataaaaaa gaggttggtat ttttgacttg gttattaagg120
ttattaaaaat tagcccttcc ttgaaatat gacatcagct ttgctgttct aaattttaaal80
ttagttgctt catcagtacc acacttccag ttctataacc aagccagttct cctcagtttt240
cccattagaa tggacatgtg ctgttcagcg tgtcatgtct gtaatgcttc atgcagagag300
tttggtcata gtattaaaga gaaaatacag tgaggtcaca atgtctccag agc      353

```

## (2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1039 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

cggggataac caaacacagc tgtttacggt ttctccctta acccatgctt tcataaaccc 60
cttcgggacag cttcccggtc caggctttct aaccacacct accccagggg tgccgcattc 120
ctgcactcagc aagtctcgag cggtccctca aaaaacttga ttgtgccata aaaatcactg 180
gggatcttgt taatacagct tctaactcaa tagatctggg agatcctgca tttctaacaa 240
gctcccgagt aaggcggagg ctgctgggtg gaggaccatg ctgtgagcag cagggcgaga 300

gtgccagggc ctgatatata ttgaaatat caccocctgaa gccatcgctg gccccacact 360
cctgtggact gatgccccag ggattcccac cccacttctg caaccccagg tatccttoat 420
tatccacccc atcccagact cccaccccag ggattgcccg tgaagacttt ggccagcaa 480
attgtgtctg ttatgtgagt gttgttttaa tcagagatgt acatgattgc caatctgcat 540
ttcttacccg tgtgaccaca ctgttacgat gcaattctag ccaaaaaaaaa actttttcct 600
agtcttatgt aaagcaata tacaatgatt ttcagtaggc ttctggaata gaaacagtgg 660
tttgaagacc ccactgcacc ctttatggac tggccccctt gagtctgaat ccccgccctc 720
tgtcacctga gacccaaccc ctgactgggc caactccagt gaattcacc atttttcttc 780
ttcagaagcg ctttctctgt tgagaccac atattttaac cttttgctcc tatccattt 840
ttaaagaatt agagaataaa ccaggccctg ttcttttccc ctgaaatccc tgccctctggc 900
ttcctaacc ccatcatcaa ggtgacagag cagtgtctgg aataggcatc ttcctttcaa 960
ctttcccaa actggccaca gataggctgg ccattgggaag ggtctttgga tttcggggga 1020
ggcaaacgtg ggggattgt
1039

```

## (2) INFORMATION ON SEQ ID NO. 85:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 330 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

agtgtattcca gcaaatgagg gtcagaaactt tcagttttatt gatggtttatt cagccgcaga 60
tgagagttta tgcgtcagcc acttcaattt ctgtaaacag aggcacaggg caaggactgt120
aaggggcaga actagttttt ctccaaaatt gcctaggcat aataaggaaa atagcacttt180
tatttcaagg aaaccgattg aatgttcaaa tgaggaagtt gttaatcaag ggcagtcgga240
tggatcaatg ggtaaatatt aggtggcgctc aaggaggggc ttatatccac tcaaaccgg300
atgttatttg gtcgggcccac gggttgaagg 330

```

## (2) INFORMATION ON SEQ ID NO. 86:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 235 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

atttaagtat tttttagttt ttaaaatgtc ttccgggtga gggaaggagc cccagccaga 60
aagcaattca atcatgggtca agtttccaac tgagtcactt tgtgagtggg taatcaggaa120
aaatgaggat ccaaaaagaca aaaatcaaa acagatgggg tctgtgactg gatctttatc180
atccattcta aatccgattg aatattgcgg gttacaaaa tgccaagggg gtgac 235

```

## (2) INFORMATION ON SEQ ID NO. 88:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 866 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```

caggaccagc ctggccaaca tggcaaaacc ctgtctctac taaaaagtaa aaaaaattag 60
ccgggcatgg tggccttgctc ttgtagtcoc acttcagtcct aagtagctgg gactacaggc120
acgtgccaca agcccagcta atgtgggtgt ttgttagag atgaggtagg gccatattgc180
ccaggctcgt ctggaacacc ggggctcaag gaatctgccc atcttcgcct cccaaagtcc240
tgagatagca ggtgtgagtc atcatgcccc gccctcctga agttactaa caattgggat300
aactgagggg agagaagtga caattccact cagtctatta gaggtctgga tataaggtag360
ccacacaata actctaaact gactcttaac cattctatct tattgattg gaggcctgtct420
tctgccagat tttttgtggc ctgagatgat accttcgaac ccttctttca ctacctttct480
tacccttaat gtgccaaagt tgaacacagga tttgatctcc tgagctactt gttcgccttc540

tgctgcgtcac caagtaatct ggttcactct tcgtctcatt catgttattt tcaagtga600
caagacattt tgggggtcaa gtctctttgg gtgttttgtt ttattgtata taaaaattgga660
ttttgtgttc cctttccatg taagacccaa cttatatgga aactcacaat cataatgtaa720
agaagaagtg aaagcctcgt gtattgtact tcaagatgcc tcctctgatg atagaaatctc780
cttgtaaaat aaataattgc attgtatctc agtcttccca tcaatattaa ttattaaata840
ttttagaatt ttttaatacc aactat                                     866

```

(2) INFORMATION ON SEQ ID NO. 90:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 846 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

ctccttgtcc aacggaaaaa acatggaagg gttaagccta aacaaccctc aaacggaact 60
ttatgccaga aaacaactac ggaataaaaa cccacaaaaa tacagagagg aacgttttta120
accttttaggg cctgcgtcct ctgcctttgg cccatcaggg tcaaaagagta ggagtgagga180
aggaagggat gggacagcat cccctgggac gttcaagtac catccctggg ctccactctc240
cagccctaga gagtggacca gccagagcac ctcgctcggg ctctcagacc tgcctgcttg300
tctctaccaaa ccttggcagg gatctaggat ccatttagtg ggatcagggt ccagtcgaata360
ccattggggc tcaataaagt tcttagaacc acagagtccta gggccagggt cccaactcat420
aggtgacgga gttccctttc aagctcgtgc cgaattcggc acgagcgggc acgagcttga480
agggaactcc gtcagctatg agttgggacc ctggccctag actctgtggg tttaagaact540
tatttgagcc ccaatggtat tgactgggac ctgatccac taaatggatc ctagatccct600
gccaaagttg gtagagacaa agcagcaggt ctgagagtcc agacgaggtg ctctggctgg660
tccaactctc aaggctggag aaggagacc aggatggtac ttgaacgtcc cagggatgct720
gtcccatccc ttcttctctc actcctactc tttagccctg atggccaaag ccagagacgc780
aggccctaaa ggtaaaaaac tcctctctgt attctctggc ttttactccc tagtgctctc840
gcataa                                     846

```

## (2) INFORMATION ON SEQ ID NO. 92:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

cgaaagcgtc ggactaccgt tggtttccgc aacttctctg attatctctg ccaaggactt 60
tgcaataatat ttttccgcct tttctggaag gatttcgctg ctcccgaag gtcttggacg 120
agcgcctctag cctctgtggga aggttttggg ctctctgggt cggattttgc aatttctccc 180
tggggactgc cgtggagccg catccactgt ggattataat tgcaacatga cgcttgaaga 240
gctcgtggcg tgcgacaacg cggcgcagaa gatgcagacg gtgacgcgcg cgggtggagga 300
gcttttgggt gccgcctcag gccaggatcg cctcacagtg ggggtgtacg agtcggccaa 360
gttgatgaat ttggaccocag acagcgtggg cctctgcctc ttggccattg acgaggagga 420
ggaggatgac atcgccctgc aaatccactt cagcctcctc cagtcctctt gctgtgacaa 480
cgacatcaac atcgtgcggg tgtcgggcat gcagcgcctg gcgcagctcc ttggagagcc 540
ggcgcagacc cagggcacca cgcaggcccg agacctgc atgtctctg tccacgaacc 600
tcacacggac gccttgaaga gccacggctt ggtggagggt gccagctact gcgaagaaag 660
ccggggcaac aaccagtggg tccctacat ctctcttcag gaacgctgag gcccttccca 720
cgagcagaat ctgttgagtt gctgccacaa acaaaaaata caataaatat ttgaaccccc 780
tcocccocag cacaaacccc ccaaaacaac ccaccccacg aggacctcg ggggcagagt 840
cgttggagac tgaaggaggaa gagaggaggg agaaggggag tgagcgcccg cccccaggcg 900
agagatccag gagctggcgg cgcgcgatca gatggagaa gggggaccca gcccgacagg 960
agacaggacc ccgaagctg aggccttggg atggagcaga agccggagtg gcggggcacg 1020
ctgccccttt ccccatcacg gaggggtccg actgtccact cgggggttga gtgagactga 1080
ctgcaagccc caccctcctt gagactggag ctggcgtctg catacgagag acttggttga 1140
acttggttgg tccttgtctg caccctcgag aagaccacac ttggggactt gggagctggg 1200
gtcgaagtgt cctgtgaccc atgaaactcc agtttgcgaa ttatagagac aatctatttt 1260
gttacttgca cttgttattc gaaccactga gagcgagatg ggaagcatag atatctatat 1320
ttttatttct actatgaggg ctttgaata aatttctaaa gcctctgaaa aaaa 1374

```

## (2) INFORMATION ON SEQ ID NO. 93:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 761 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

gacctgatggg ctggagccag actgtggtct gaggaggaga cacagcctta taagctgagg 60
gagtggagag gcccggggcc aggaagcag agacagacaa agcgtttaga gaagaagagal20
ggcagggaaag acaagccagg cacgatggcc accttccac cagcaaccag cgccccccag180
cagcccccag gcccgaggga cggaggactcc agcctggatg aatctgacct ctatagcctg240
gccccattcct acctcgaggg tggaggccgg aaaggtcgca ccaagagaga agctgctgcc300
aacaccaacc gccccagccc tggcggggcac gagaggaaac tggtagacaa gctgcagaat360
tcagagagga agaagcgagg ggcacgggcg tgagacagag ctggagatga ggccagacca420
tggacactac acccagcaat agagacggga ctgcggaggga aggaggaccc aggacaggat480
ccaggccggc ttgccacacc ccccacccct aggacttatt ccgctgact gagtctctga540
ggggctacca ggaagcgcc tccaacccta gcaaaagtgc aagatgggga gtgagagggt600
gggaatggag ggcagagcca ggaagatccc ccagaaaaaaga aagctacaga agaaactggg660
gctcctccag ggtggcagca acaataaata gacacgcacg gcagcacaaa aaaaaaaaaa720
aaaaaaaaatc ttgttaaaaa aaaaaaaaaa aaaaaaaaaa a

```

## (2) INFORMATION ON SEQ ID NO. 94:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1825 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

agggaaagcta gtagcggacc ggaagtgagg caccctcggg ctcgagacag cggcgacgtt 60
taaaagctgag cgacccaagt ccactggaga cggctcagctt ctccactcag gctcctccag 120
cccgaagccag aagacccccct cccccagaat tctggggggcc gatggaaagg agccgagtgca 180
gatcgcgagg taccacagag cgacagacgg gagcgacagg gagtggccag aagccccgcc 240
cctaggagtg atcggaagg ctcacccatc cgggtgagga acccgagga ccgctccgg 300

gcggaagcgc gaccatggct acgccccctg tggcgggtcc cgcagctcta cgcttcgccc 360
ccgcggctag ctggcaggtt gtgcgcggac gctgcgtgga acattttccg cgagtactgt 420
agtttctcg arctctgcgc gctgttgccc ctggcttggt tgcctaccgg caccacgaac 480
gcctttgtat gggcctaaag gccaaagtgg ttgtggagct gatcctgcag ggccggcctt 540
gggccccagt cctgaaggcc ctgaatcacc actttccaga atctggacct atagtgcggg 600
atccccaggc tacaaggcag gatctgagga agattttgga ggcacaggaa actttttacc 660
agcaggtgaa gcagctgtca gaggtccttg tggatttggc ctgaaagctg caggaaacttg 720
aacaagagta tggggaaccc ttcttggtcg ccatggaaaa gctgcttttt gactacttgt 780
gtcagctgga gaaagcactg cctacacocg aggcacagca gcttcaggat gtgctgagtt 840
ggatgcagcc tggagtctct atcacctctt ctcttgcttg gagacaatat ggtgtggaca 900
tggggtggct gcttccagag tgctctgtta ctgactcagt gaacctggct gagcccatgg 960
aacagaatcc tcctcagcaa caaagactag cactccacaa tcccctgcca aaagccaagc 1020
ctggcacaca tcttctcag ggacactctt caaggacgca cccagaacct ctactggccc 1080
gacacttcaa tctggcccc ctaggccgac gaagagttca gtcccaatgg gctccaacta 1140
ggggaaggcca taaggagcgc cccacagtcg tgcgtgttcc ctttaggaat ctgggctcac 1200
caaccacggg catatctaag cctgagagca aggaagaaca tgcgatatac acagcagacc 1260
tagccatggg cacaagagca gcctccactg ggaagtctaa gagtccatgc cagacccctg 1320
ggggaagggc tctgaaggag aaccagtggt acttgctctg cacagagcaa aaggagaatt 1380
gcttggtatt ctacatggac cccctgagac tatcattatt acctcctagg gccaggaagc 1440
cagtggtctc tcctctcttg tgcagctcgg tcattacat aggggacttg gttttagact 1500
ctgatgagga agaaaaatggc caggggggaag gaaaggaatc tctggaaaaa tatcagaaga 1560
caaatgttga cactttgata cccactctct gtgaataacct acccccttct ggccacgggt 1620
ccatacctgt ttcttctgt gactgtagag acagttctag acctttgtga tagaactaaa 1680
atgctctctg tactctagtc tcctgcctcc tcagctctgc aagtagttta gtaggaaatga 1740
agtggaaagc caggcttggg ttgcctaact acactgctaa aaattattgt aatccttaat 1800
aattaaactt cggatttgtt aaaaaa
1825

```

## (2) INFORMATION ON SEQ ID NO. 95:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1374 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

ccgggattcg ccctccgggg agcgattggt cctcggggagg ggcggggagg tggacgcggg 60
taccggcggt cgctcgggtcg gcagcctttg gtcagttggc agcggccaag gcgctgcggg 120
tcgggtggcg ccattgctgtt ctgcagcttc ttccggggcg aggtttttcca gaatacattt 180
gaacctggcg tttaactgtg tgccaagtgt ggcctatgagc tgttctccag ccgctcgaag 240
tatgcacact cgtctccatg gcccggcggtc accagagaca ttacgcgcga cagcgtggcc 300
aagcgtccgg agcacaatat atctgaagcc ttgaagggtg cctctggcga gtgtggcaat 360

gggttggggc acgagttcct gaacgacggc cccaagccgg ggcagtcocg attctgaata 420
ttcagcagct cgctgaagtt tgtccctaaa ggcaaagaaa cttctgcctc ccagggtcac 480
taggcgggca gccacacacc accccagacg gccaccacac tgaggccaca cgttggccat 540
tccaccttgg agttggaacc ctgggcgtcg agacaggaaag gtaggttgaag 600
catcaggaca ctcaccaagg cccggctctg aacaagacct ttctgtttct tggaaaagag 660
actcatttgc tgatggttca tgcctttctg tgggacaggc ctgggctgtg cagccacact 720
gtcggctgag tttagccccc gctcactcta ggtgcctcca ggaagtgagc cctgggtgca 780
gctggtctct gaatgacgtt acacccctac cttcttttcc tggccctgtc tctggactct 840
ccctgtgtag gcccaattcc aagacagact ctgctcctca ccgaagctta gcccacac 900
tcccaggctg cttaggagac agaattgaaa cggaggcccg ccctgccagc cgccttgccc 960
ctggtaccgc catgatccgc tctggtcaaa cccttcaggg tggggatggt 1020
ctgtgacctg ctgggaaggc aggcctatgg ggcacaccc tggcctctcg tccacgaggg 1080
gagaaacctc aacctgttt cacaatctgt gcggaagtag cttgcctcac ttctgcttag 1140
gaaaacggct gttgctccat aactctaacc agcacaggcg tagggcctcg agtgacacac 1200
tgacgggagg ccttcccaaa ggtgtggtga ctgtgcctta ctgtacatgc tcggaggcct 1260
ggccatatag gaggggtggg gatgctgaaa tcacccccca tcttaagtga ttactttctg 1320
gagtaatcag gtggaatccc atagacaaat gaaacattca gatgtaaaaa aaaa 1374

```

## (2) INFORMATION ON SEQ ID NO. 96:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2615 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

cttgggaagc  tctctggaatct  ttgtcaacct  gactgtgcga  ttctgtatct  tgggaaaaga  60
gtccttttat  gacacattcc  atactgtggc  tgacatgatg  tatttctgcc  agatgctggc  120
agtttgtgaa  actatcaatg  cagcaattgg  agtcactcag  tcaccgggtg  tgcctctctc  180
gatccagctt  ctgggaagaa  attttatttt  gtttatcatc  ttgggcacca  tgggaagaaa  240
gcagaaacaa  gctgtgggtt  tctttgtgtt  ttatttgttg  agtgcaattg  aaattttcag  300
gtactctttc  tacatgctga  cgtgcattga  catggattgg  aaggtgctca  catggcttcg  360
ttacactctg  tggattccct  tatatccact  gggatgtttg  gcggaagctg  tctcagtgat  420
tcagtcocatt  ccaatatcca  atgagaccgg  acgattcagt  ttccatttgc  catatccagt  480
gaaaatcaaa  gtttagattt  ccttttttct  tcagatttat  cttataatga  tatttttagg  540
ttttatcata  aatttttgct  accctttata  acagcgcaga  cggcgctatg  gacaaaaaaa  600
gaaaaagatc  cactaaaaag  aaagattttg  atggcttctt  gccagtttga  gccataatctg  660
attctcacag  tttttacctc  ttgaaccaat  gtaaaagttt  ttttaagtgt  aaagtattaa  720
attctcagtg  aggtctatct  ccttttcccc  agtaaacatt  ctgaattttc  tgtttatctt  780
ttgtagtagt  tgcattgacat  ggtattctct  tatctgatga  gagggttcatt  cttgtgtatt  840
cagttaatga  caccaaaagg  ctacgcccac  cccaacccta  tctcatgttc  agtctgtcta  900

atacatgcca  gagatttttt  tttcaaaaag  tgctttatcc  ctacaatgta  ctgacagctc  960
ttacagttga  gatttgttct  tttcagctat  tgcttgtgaa  aaaaagcaag  actatgtcac  1020
tctatagaag  gctgtttaaa  tgactcaggg  aggaatttaa  tattctgtac  ctaagggggt  1080
acttgtttaa  tgggagtggc  ttgacttttt  gaaaatcaag  tggactgagt  catgtgataa  1140
acatttctaa  gagtggggct  agagaacata  ctttacctct  gacatccttt  gccctaaaaa  1200
catctattat  tatagtgtct  agcagttgtg  gcattgaaga  ggcgcagaat  gctttgaaag  1260
aaaactaatc  gaattcttga  acatcatgat  catgccatcc  ttaagcaaat  caactatttt  1320
caaacactgaa  gaaaaatgaa  acattattta  gaaaacaatg  agattacaag  ttccaaactc  1380
agccaggaaat  gtggctcaca  cctgtaatcc  cagcactttg  ggacacactg  gtgggagcat  1440
cgcttgaagc  caggagtcca  agacacagct  gggcaacgta  gtggagacc  ctatctctac  1500
aaaaataaaa  aaaaattagc  ggggtgtgat  gcacacacct  gtttgtccca  gtaactcaag  1560
aagctgagat  gggaggatcc  tgagctcagg  aggtcaaggc  tgcagtggag  cgagattgtg  1620
ccactgcact  cgacgctggg  gtgacagtgc  aagacctgtc  ctcaaaacaa  accaaaaccac  1680
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aaataattga  gtatggctaa  cacacctcca  aactgtaaag  ctgtgcacaa  acataaaaaa  1860
tggcagcctt  ccatctcctg  cactgggtga  gtccatttac  ttgtgtactt  gttctagtga  1920
gtgggtggag  tgtatcattt  tgaatatgac  tcaaaaatac  ttocttctgc  tgcgtgtcag  1980
tttgcctttt  aaacctgtct  gcagtaggac  actgaaaaaa  gcaagaactt  cgggtggaac  2040
accctgtgat  ccttttaaca  ggaatttctg  caggaaaact  acaaaaggaa  gaactgaaa  2100
tttagacata  cagttggcca  ttgtaaaaaa  ctacagtttc  cttctcatac  ttccaagtta  2160
accaagtaaa  ataatgtttg  gagttaacact  tgcataaaag  aatttaagga  gtgataagct  2220
tttctgttct  gccattccca  acattctctg  gggaaaaggag  actcaatgag  ttaataacta  2280
ttcactgagc  ccaagatgga  aacttgggtt  gacctaaaaa  atctgattaa  tatagtgct  2340
ctgatttctt  aaaaattcgt  tgcatgtga  gataattttg  acgtgttaat  caacctgtca  2400
tacttgtttg  tattgtattt  tgatatctct  gcagctgact  acgtgttaat  gggcagatca  2460
gcaaacccct  tattgtctgc  tgagaaagtg  aaagattgtg  tatttctatt  aaacatttta  2520
caatcaaaaa  aaaaagaaa  aatagaagaa  aaagg

```

## (2) INFORMATION ON SEQ ID NO. 97:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 508 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

```

gttggcagaa acccggtatc cgggtccggg gggcctccat cagcaagctc cagtgcctacg 60
tgtccctggc atttttagtg tcggttgggt aggcagtcac ggatcaggta atgcagtttgl20
ttgagccaag tcggcagttt gtaaaggact ccattcggct gggtaaaaa tgcactaaac180
ctgatagaaa agaattccag aagattgcc aagcagcagc aataggattt gctataatgg240
gattcattgg cttctttgtg aaattgatcc atattcctat taataacatc attgtttggg300
gctgaataca ttttggaaga gagtttttca tcttagagat tgggtgaacaa gtgtgagggg360
gtgagaaact cacagaatac aaatttgcc gtatgttttg tgggtttttt tttttctctt420
caagatgttt tctatttcta aattaaagta atttcaaagt aaaaaaaaaa aaaaagtcca480
cgcggcgcgc aatttagtag tagtaggc

```

## (2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3588 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

ctccgtctca aaaaaaaaaa aaaaaaaaaa aaaaggggaag ggaatcccat tttgtgatga 60
tttgggcaca ctacttgagc tgaggctagc agtcacatga ttttggctgt ctctgacctg 120
aagcttttga agtaagggtta tgtctcttcc ctgaagcttt gtttatagtg gtaatttggg 180
gagtttgagc tttgagcttg tcttagaaaa taagactgtc cacctgggga ggggagctta 240
tagggaaacc gtgttaactc agaagtgtga agaaagtgtc tttagccaac aaaagttaaga 300
ttactatcta gaaggtggaa agaagtcatt gcttctgttc ctccagcagt cagttgacct 360
taggtttcct ttggtttata tcccagtttc ttaatactaa aacttatttg acttccatct 420
aggaagcaca caaaaaaaag gtcatttaaa accctggata taggctttaa agatatacaa 480
aacagcagca ttgtcgtttt gccaggttca tcaccatttt gatgtgtcac ccatccttcc 540
accctccctt tccctgcccc aagcctccca gccaggccag atgtgaagat ctacttaaat 600
actgtttcag agaaccattaa tcttctgata gaataattat ctactaaatt gcttattatc 660
tgtgactaac ttgcagagaa catctcaaca gtgcagtaaa atagctctcc tagacttgag 720
cttccagcga gccattttag tcaactttaa gccctttgtg aattctgagg aaaaaaagca 780
agatgcctca atgccaatgc tggggccataa gattctactc cctcctctgt aggggtggggc 840
cgctgtctca gcttttggaa atcattttgc cagttaattt gctgtgaagt cctttaaaga 900
agtcgtcctg atctgagctt gcttttctga gcactttgtg gctgaatttg aaatggtaag 960
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agtttctcag gttaaacctt tgtctttaac ctccctttgt tgtggagaaa atgtgtcact 1080
aatcagttgt ccaagggata tctagctttg gttactcagt tctctgcagc taacagatat 1140
gactttatgc aggggaagga gaggctgatt atggagacac ccaggaacag taataagaag 1200
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aaagtgtctg agtaaaaaag agacttggag gccctttgtc taatgagcaa gaggcttgtg 1320
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cgctcacccc atccctcgtc actgggagca tgtttgtcca gaatttctc agaggactct 1440
cccttcaaaa atccaatttg ctccagaagt gttgttttag ctctgagaat ctcaactctt 1500

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aaagaataca gtatgtagta cagttttgta aatgtcaggt ctgttctgtt gttttgtgat 1680
ctgaagactg tcaaacctggt cgataatcaa agaaaaggtt ggttggttaga ataaagtaaa 1740
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tcaggtttgt gagaactggt gtaaaatgga attagagcta gtgtctctca cctctctagg 1860
tgtatcaagag agaggaagtg gaaggccagt agtagcatct tcataacttac ttttgccaga 1920
ccagcctcca ttttcaaagac ttgtctctcc atctcatcca atgacatggt caggagtagg 1980
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cagcttaagg gtttttaagt ttcttcacga ttacctccac tccactccat tactatcagc 2100
atcagaaaag ttaacatccc tgggaccatt ctactttata aagagatgaa ctatgtgtgt 2160
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tcttccagg gaaccccggt gggtgaggca aagttagccaa gatgtattga ttaagtgttt 2280
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cgtaaatggc caagtgtgag aatatctgtg gaactgagac agagagccag ggcacctagt 2400
accacgggac cagtccctgt gggaatcaca cagtgtctca gactagactg ctctatccca 2460
ccagaaactc gctgtcgttc atttccatca ggaccaccca ggaagcaaaa taagttagcc 2520
ttctcatcat tagtgcactt aatctcttgg gttgcaggat gagagcatat atagatctcc 2580
tgtttagaga gtgtgttcat aattgtagaa aggggataaa aatggaataa ccaaggaggt 2640
gtgtcatttt ttaagaggat ggcaaggtag acctcaaat agctcaacaa aactgggaat 2700
ccaaggaatt gtgcttgtag ggaaagagag gtcatgtgtg gctcttaaac ctctggcac 2760
cttctgcggg ttataaaaaa aggaagctga gtaaaattgc ccttaccccc atcccaaatg 2820
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tcttgcctgc ctcaagggtg gctcttcccc cgtgtcttca acgggaagatt caagggaagt 3000
tttgcagcac tctctggagc tgaggggagt gaaatttggg ccagagaaag cgggaagaaa 3060
tagtttctct gtttcccttt ctcgaggtgg atgtctccag gcttcttcca caccctcttc 3120

```



```

tcatgggtgc ggctggcagt acagtcaggc tgtggaggag ggctgagaag aaaggggcac3180
tgggtccagcc ccaggttttgg tctgagacag gtacacagca gataccatcc cacccttcctc3240
tctaaagaac aggccagcca cacatataac cctttcccta ctttactaat gtatccctta3300
tgtgtgtacca gcaatggagg acagggcagc ttaccocctg ccactctagag agaatgttgt3360
tattacccgtt aaaacttgac caccocccata tcccaactcct ttttgtaaaa acaaatgctt3420
aaaactgtga gcttgccgtt cctttctatg tgttaatcag ttctcttcca tttgagctgt3480
gtggggaggga agggcattga aattgtaggt tgtaatcttg tgccaaacca taaaaaccag3540
tatttcacac acaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 3588

```

## (2) INFORMATION ON SEQ ID NO. 99:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1218 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

tgggtggcgtt taaataacaa atctgctaaa gttaggcaac aggcagctga cttgatttct 60
cgaactcgtct ttgtcatgaa gacttgtcaa gaggaataat tgatgggaca cttgggtgtt 120
gtattgtatg agtatttggg tgaagagtac cctgaagtat tgggcagcat tcttggagca 180
ctgaaggcca ttgtaaatgt cataggtatg cataaagtga cccccaacta taaagatctg 240
ctgcctagac tcacccccat cttaaagaac agacatgaaa aagtacaaga gaattgtatt 300
gatcttgttg gtctgtattgc tgacagggga gctgaatatg tatctgcaag agagtggatg 360
aggattttgt ttgagctttt agagctctta aaagcccaaa aaaaggctat tctgtagagcc 420
acagccaaca catttgggta tattgcaaaag gccattggcc ctcatgtatg attggctaca 480
cttctgaaca acctcaaaag tcaagaaaag cagaacagag ttgtaccac tttagcaata 540
gctattgttg cagaacaacg ttcacccctt acagtactcc ctgccttaat gaatgaatac 600
agagttctct aactgaatgt tcaaaatgga gtgttaaaat cgttttctct cttgtttgaa 660
tatattgttg aaatgggaaa agactacatt tatgcggtaa cacogttact tgaagatgct 720
cttggtgata gagaccttgt acacagacag acggctgatt cagtgtgaca gcacatgtca 780
tttgggtgtt atggaatttg ttgtgaagat tgcgtgaatc acttgttgaa ctatgtatgg 840
cccaatgtgt ttgagacatc tctcatgtga attcaggcag ttatggggag cctagagggc 900
ctgagagttg ctattggacc atgtagaatg ttgcaatat gtttacaggg tctgtttcac 960
ccagcccgga aagtcaagga tgatatgttg aaaatttaca actccatcta cattggttcc 1020
caggacgctc tcatagcaaa ttaccocaa gaatcacaag atgtacaaga ccacctaat 1080
atccgggtta tgaaccttgg cctatagctt agtaatttta agtgggttat tttgtgggtt 1140
aatgccactt gcttcacacc ttaaaactgc tttgagtttg tgggtgtacc tttaaacatg 1200
ca;atcagtg gtgactgg
1218

```

## (2) INFORMATION ON SEQ ID NO. 100:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1303 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

gtgctcaaga agtgccttga gttgggtgac agtgccatgg ccagcaagaa tccagattt 60
cagggttttat tacaaaaatgt aagtgggtcac ttggcgattt tgtagtacat gcatgagtta 120
cctttttttct ctatgtctga gaactgtcag attaaaacaa gatggc aaaag agatcgttag 180
agtgcacaac aaaatcacta tcccattaga cacatcatca aaagcttatt tttattcttg 240
cactggaaaga atcgtaagtc aactgtttct tgaccatggc agtgttcttg ctccaaatgg 300
tagtgactcc aaataatggt tctgttaaca ctttggcaga aaatgccagc tcagatatatt 360
tgagatacta aggattatct ttggacatgt actgcagctt cttgtctctg ttttggatta 420
ctggaataacc catgggacct ctcaagagtg ctggacttct aggacattaa gatgattgtc 480

agtcacattaa accttttcaat cccattatgc aatcttgttt gtaaatgtaa acctctaaaa 540
atatgggttaa taacattcaa cctgtttatt acaactttaa aggaacttca gtgaatttgt 600
ttttattttt taacaagatt tctgaaactga atatcatgaa ccatgttttg ataccctttt 660
ttcacgttgt gccaacggaa taggggtgtt gatattttct catatgttaa ggagatgctt 720
caaaaatgtca attgtcttaa acttaaatca cctctcaaga gaccaaggta catttaccct 780
attgtgtata taatgttttaa tatttgtcag agcattctcc aggtttgcag ttttatttct 840
ataaagtatg ggtattatgt tgctcagtta ctcaaatggt actgtattgt ttatatattg 900
accocaaata acatcgtctg tactttctgt tttctgtatt gtatttctgc aggattcttt 960
aggctttatc agtgtaatct ctgcctttta agatatgtac agaaaatgtc catataaatt 1020
tccattgaag tcgaatgata ctgagaagcc tgtaaaagg agaaaaaaac ataaagctgtg 1080
tttcccatata agttttttta aattgtatat tgtatttgta gtaattctcc aaaagaatgt 1140
aaaataggaaa tagaagagtg atgcttatgt taagtccata cactacagta gaagaatgga 1200
agcagtgcaa ataaattaca tttttcccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagt 1260
atacgttgga atgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1303

```

## (2) INFORMATION ON SEQ ID NO. 101:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2333 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

tgaaaatgc ggacagtata ttcagaaagg ctattccaaag ctcaagatat ataattgtga 60
actagaaaaat gtacagaaat ttgagggcct gacagacttc tcagatacgt tcaagttgta 120
ccgaggcaag tcggatgaaa atgaagatcc ttctgtggtt ggagagttta agggctcctt 180
tcggatctcac cctctgccgg atgacccagc cgtgccagcc cctcccagac agtttcggga 240
attacctgac agcgtccccc aggaatgcac ggttaggatt tacattgttc gaggcttaga 300
gctccagccc caggacaaca atggcctgtg tgacccttac ataaaaataa cactgggcaa 360
aaaaagtcatt gaagaccgag atcaactcat tcccaacact ctcaaacccag tctttggcag 420
gatgtacgaa ctgagctgct acttacctca agaaaaagac ctgaaaattt ctgtctatga 480
ttatgacacc tttaccgggg atgaaaaagt aggagaaaca attattgtac tggaaaaaccg 540
attcctttcc cgctttgggt cccactgcgg cataccagag gagtactgtg tttctggagt 600
caatacctgg cgagatcaac tgagaccac acagctgctt caaaatgtcg ccagattcaa 660
aggcttccca caaccatccc tttccgaaga tgggagtata atcagatatg gaggacgaga 720
ctacagcttg gatgaatttg aagccaaaca aatcctgcac cagcacctcg gggccctga 780
agagcggctt gctcttcaca tcttcaggac tcaggggctg gtccctgagc agctggaaac 840
aaggactttg cacagacccc tccagcccaa catttcccag ggaaaaacttc agatgtgggt 900
ggatgttttc cccaagattt tggggccccc aggcctcctt tccaacatca cccccggaa 960
agccaagaaa tactacctgc gtgtgatcat ctggaacacc aaggacgtta tcttggacga1020

gaaaagcattc acaggagagg aaatgagtga catctacgtc aaaggcctgga ttcctggcaa1080
tgaagaaaaat aaacagaaaaa cagatgtcca ttacagatat ttggatgggt aagggaaatt1140
taactggcga tttgttttcc cgtttgacta ccttccagcc gaacaaactct gtatcgttgc1200
gaaaaaaggag catttctgga gtattgacca aacggaattt cgaatccccc ccaggctgat1260
cattccagata tggggacaatg acaagttttc tctggatgac tacttggggt tcttagaact1320
tgacttgcgt cacacagatca ttctctgcaa atcaccagag aatgtcaggt tggacatgat1380
tccggcacctc aaagccatga acccccttaa agccaagaca gccctccctct ttgagcagaa1440
gtccatgaaa ggaatggtggc catgctacgc agagaaaagt ggccggccgg taatggctgag1500
gaaagtggag atgacattgg aaatcctcaa cgagaaggag gccgacgaga gggcagccgg1560
gaaggggcgg gacgaaccca acatgaaccc caagctggac ttaccaaatc gaccagaac1620
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taagtgggct atcatcggct tgcctgttct gcttatcctg ctgctctctc tggccgtgct1740
ccctcactatc ttggcgaact atttgtcaat gaagattgta aagccaaagt tggtaacaaag1800
gcaaaaggctt catttccaaga gtcatccagc aatgagagaa tctcgtcctct atgacccaac1860
atccagtgctg attttgtgtc tgagaccaca cccagctagc aggtttacgc atgtccaccca1920
gccccattga tttcccagagg gtcttagtcc tggaaaagta ggcccaacaa caacgtttgc1980
atcatgttat ctcttaagta ttaaaaagtt tattttcaa agtttttcaa2040
aaaaattttt caagtggtgct ggttccattt aaaaatcatc tttttatatc tgccttcgggt2100
cttagacttc agcttttggg aattgctaaa tagaattcaa aaatcctctc atcctgaggt2160
gatataactt atatttgttaa tcaactgaaa gagctgtgca ttataaaatc agttagaata2220
gttagaocaa tctttattta tgcccacaac cattgtcata ttttgtatgg atgtcataaa2280
agtctattta acctctgtaa tgaaactaaa taaaaatgct tcacctttaa aac 2333

```

## (2) INFORMATION ON SEQ ID NO. 102:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1377 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

cattactgtt atatgagaaa catttttagta atttaataaa aggataatgt ttatttataaa 60
aacctgactt ttccagagta attttgtttt gcacattcat gttttattgaa gtggactaat 120
ttctataaat caaatcagag ttaaatatta aaaatttgtt aaatacaatt gacataggaa 180
ttacattaaa atattaggaa gaaacaagga caaattttaga ctttgaatcc gaagagataa 240
agccttactt acttttcaaat ggagagatga tgaaaaccca ctcatcagtt ctttcagaac 300
aaaaagacag tcactgtgata agagtatgac atggatgaaa tgccttcacag gggccttgga 360
catctttaat ttctgagatt atgtgaaaga ggtggacttt acagataatg gacgagaagc 420
caacattagt aaaaggaatc ccaacttctt cccatagaat tagaaacatg tgaagtaca 480
ataaacttct tgttcaaatc accagcatca gagagcttcc catttgcacg tagaccttga 540

atttatattt attgacaaag ttctaatttg tatgtatatt ttgtgcatat tcaccaataa 600
cagttataat taattatgtg ttatagttaa tatatgcacc taccttcttc cgttagtgtg 660
tcagtataat tgttattttg tcatttttcc aaagagagtg ttgtagggtt tccctgtagt 720
tcttccttta tagcttttct tctgataacc atgacttcag gagcttttaa atcatctatc 780
ttgcatttgt gtctggcgga gaactagcca tcagcctcct gaagcctgcc atcattgtta 840
atattgaggac tgggctgtct tggggctcag aaggtaaaaga actatttgag cagatgtgtg 900
tgggtggcac tggattccac ccaactgcca agttagtatt gtttagagatt tcattttaca 960
acacaaaaat aagcctgtgt caaagatttt aaaatcoatg aaagttaaaa tctagaaaagal 1020
ccttagagaa ccagccaacc aactctctca tttttaaagt gaaggattca tagcacagat 1080
tacttgccca agatcatcca ggaacgaaga caagaatcca aatgtacttg gggacaagaal 1140
ttagtcccca aattcagtggt tcttctcagt attaaacatt gcccctttcg acaaattttg 1200
gatttcaatc ttggtatatt tcagttaaacc tgctgattta ttaggttact ggttagatga 1260
cattagaatg tagatagcgt gcacgcctatg atagactctg ctaagacatg ttcccagtg 1320
ccagcagcaa tgtagatatg tgtgacagtg gtcattgtaga agttataaag cagagta 1377

```

## (2) INFORMATION ON SEQ ID NO. 103:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 315 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

ataaggaatg agaagaaagg ctgtgtctta tcagtaggtg agatggaact ggtcctggta 60
gtgttgagac aggacaggca cttagtctctg atgctgtggt cctttgtgat agtagagcac120
cggggttaac caccactcct ttaggctact tgtagtgaca acagaagtaa aatatttcaal80
ttatttaatt tagaatgtta tgttttactg gaacctgcaa tatgcatgta cagaattaat240
aatttttact ctttttggtca agttatacta aggcaaaagg agtggattca aaagtgagac300
attgacaggc cattt                                     315

```

## (2) INFORMATION ON SEQ ID NO. 104:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2355 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

atgatcatgc cactgcactc catcctgggt gacagcaaga tcttgtaaaa aaaaaaaaaa 60
aaaaaaaaac gagtgaaaaa ggaagtaga aggcagctgc tggcctagat gttgggttgg 120
gaatattagg tgatccctgt gagatcttgg atccagagca atttcttttag cttttgactt 180
tgccaaagtg tagatagcct ttatccagca gtatttttaag tgggggaatgc aacgtgaggc 240
caactgaaca attccccccg tggctgcccc gatagtccaca gtcaagggttg gagagtctcc 300
ttccagccag tgacctaccc aaaccttttg ttctgtaaaa ctgctcttga aataccggga 360
agccccagtt tctcacgtgg ttcttagctt cttcagaact agcccaaat aggaagtcca 420
gaagcacatg atgggtgaaaa acctaggatt tggcagcctt ccagaatgtg atggaatctg 480
aggggaagatt tatgttttgt tttggaggat agctcaagtt gaattttctt tccagccagt 540
taccttttca acctacccat accttgtaaa actcttacac aaatacttag atatttatta 600
gatagccctg aattcaactct aattataaac agggagtgtg aactgcccc agatgttctt 660
gggtcgggta aaagcagctg gagtgaagca ctcatcttcc ataaaggtaa caaagggcag 720
ctcagtggtt actcaagctc aaaaggggtt ttttaagagc aagcatttgt taagtctgtg 780
tatactggat tgggaagtgt ttcagcacat tcttttttag tggagtgaia gttctgaagc 840
ccccctttta ctctctcttg gtttttcatt ataattggta gccatctcat gaactgtctc 900
tgactgttgt ctcttttggt tcatgtgatt gtgagcttgc tttctgactt gcatttctga 960
ctttatcctg ttgttaggaa gatagaaact aggttttgaa agatatacat attcaagcga1020
gggatttttaa agtaaaagat tattttattc gaagaattca aaagataaca gattatttgc1080
ttatgaaga acaatatagt ctgggaatcc cagaaatgtc agccaaaggt ctaagaagtc1140
atctctctca aatactttta taaagaagta tttcgaggag atactgtgcc aaaaaggtt1200
gactggctcc cagattccag ttatttttaa aaagcaactt accactaaat ccttgagtct1260
ccatagagta acagttaaag aactgatgta acagactctc ctctcaaaag atctctctgt1320
gaagagacta tcagcggcag cattctccag ggaagacca tccccagtg ccagagcttg1380
ctccctggag actaaagatt gcaacttttt gtatgttttt gtccaaatgc aatccccatt1440
ctgtgctctc tagcatgcag tttagatttg acaaaacaaga ttcttaagga atgactttat1500
taactataac atgggtacag ctattatata aatatatat ctgggtatag ttctaataat1560
gagatgttgt gtgcaatgct ggccgtgggt ggtctgtgta atgctttaac ttgtatggag1620
gagggccagg tcagagctga gatgtggcct gaacctctcc tgatcagatc cttaattta1680
gaactgtcaa gatgtcactt tctccccctc tgccttttag tggatctgta catatactca1740
aaacagtaat tctctgggtc catcatcaac tgctaattct gtatttataa agaattttca1800
gatggacatg tacaaaattt aactcaaac atccccagtc cagatacagg gcagcgtgta1860
ggtgaccaca ccagagcctc agcctcgggtc ctcttcagcc gtccgggatg gatccaggca1920
tttctcttaa atctcagagg tagcagtaaa cttttcagta ttgctgttag caagtgtgtg1980
tttgccaata gatcacctat atactaatgt gccaaagtaaa tggttcatct acatctgtct2040
ccactgttgt cccacgggtg ccatgaagtg tgtgaggagc cctctcatct gagggatgag2100
tgctgcgttg actactgcta tcaggattgt gttgtgtgga atattctatc acataaattt2160
tatatgcaca gtaatttccc tttttatag tcaagtaact atttgtaaaa gttatactca2220
caaattatta taatgattac taatatattt ttccatgttt tcatctgctg aataaaact2280
gtttacacct gttaaaaaaa aaaaagttaa aaggaggagg tgggaaaaaa aagctggggg2340
ggggggcccg tagcc
2355

```

## (2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1339 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

attcggcacg agcatgaaac atgctcattt tacctaacag taaacaagta tgttttgata 60
gatatctggt aatatgccta tagtggttaag aaatggacctt gagggtccag gagatttcat 120
tttattccacc ctggtcagat acaataaagg ctatgagtat aaatacataa ctccctaacc 180
agggtgtaggg catgttcgat aatatcaaat cttttgatgc tggaccocaag agaggaaaag 240
ttgtagctaa atgttgattt acttataact agacgtctat gtgagaaaaa atagtgtatac 300
atataatga tatgcagaag tcaacttttt tatcaggctt tattctcctt acaaaagccac 360
agttttaactg tctgcaaacag ttggtttatg ttaatgatag acaaataccg agtgttttgtt 420
actttttcca actaccactg taatgataat cttttctcac tatatacatg caactctctg 480
gcttcaatttc catgaagctg tttcaataata ttcaagtatac ttgtctctta atgctgtcttc 540
tgttaacagt gatctctttc tttttttcat tcttatactt tcattagttc atcataaatc 600
tgtccagttg aggcctcagg accacggcat gatttcatga ctccgaagta ttttacagaa 660
acattttttta aataaggaaa atattttata taccagatgg ttccacaagt atggctcata 720
gctagttttt tttttctctc taaaaaaatgt caggttttta aaatcattta ccttattaaa 780
atgaaaaagt ccataactta cttttaaagg aaagacctga cttgtctttt ctctatttag 840
actgtttttt tactttacta atcttttaaac tatcaggaaa aaaacccaaa ctttatacca 900
atgatttagt aattttgagg catagggtag cttacgtagt ggaggatgtg ccaaatattc 960
tcttcaaatg ccaccttctc aatttataac taaaatagtg ttatctgact aattcctctg 1020
aattttgatg taagatctat ataggccccc aaaatgatcg tagtacatgc cagtcatctc 1080
tcagtgaaat aaatacaata ccagagtaca ttatgggttt tattgctttc ttttatggta 1140
gacctgttaa tggggaaaaa atacatcaaa tcaaatagaa tcttatactt gtatgtttaa 1200
atagagcact tacctgaagt cagtggcctg gatcatagcc ctggatcatt tccacgtctg 1260
tcctgtgctg ggtggacctt ggacaaggcg ctgcagtagg tgatggctga gagcccttcc 1320
ctgttcccaa gtgccttgt

```

## (2) INFORMATION ON SEQ ID NO. 106:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3751 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

gatcgcgagc ggccctttgga atctattgtg caaaagaagt ttcatatttg ttacttagac 60
ctaaagatcac ttattaaaaa tctctatttt ccccaagccc agcaaacggt gactctcggg 120
caaacctgaa aaacctgaaa tgccactttc atgcagtttg tttgaagtta agtgggaatc 180
tttcaaatga cgaagctgac agaactcagc accaagggtc cgtattctgt agtagctgt 240
aaaatggaat atttttaaat gaaggcaaat aagtacttaa aagtgcagctg agcaataaaa 300
tggtccaata ataggttaaat gcaacagaaa cagaaggaga cctggtttgc ttatgccttt 360
acctttacat ggaaataaat cccaatgcac atcttatgta aaccataaag gaagggaaat 420
aaacctcgtc atgtctccatg ctgtcgagtg tccctttggt atctctgtga gacagagaag 480
cctattttgt tttgttttca gcatctttct ctgatgtacg tttttaagga ttttgtaaat 540
gctgttttca gtgttttaaat tagtgctatt tttccttggt tttaaaaaat aatctctgac 600
tgtattctac tatgtccata cagatgtttc aaatcgacag ttttattctt agactcagt 660
gatccaaagt gtataacca tatataacca ttttacctga atcatttagt tttttaattc 720
atttactaat gctataaaat ttcttatatt accccagtaa ttgcatcag ctggtttata 780
tactaaagca acatgttttg atgagtttct tacatcttta tcgaggaagt ggggttaggaa 840
aaaaacatac attgtaaaaa tgagtttgct grattatact tttttcttg agtattagt 900
gtattactaa tcatagtgt attcaactgc tacttaagct caaggtacct gtatttttaa 960
tccacttaatt tttttttagt tgggaaaatg atttcaagtc tttttataga tcaactattt 1020
tgctgaagta aaattgacct catatacaaa ttaggcgaaa ttgaagcaga 1080
aatctaggaa gtgtgtgctt ctgttatgtt gagttttgct tcagactaac taatgcatac 1140
gaattctgac gtgttgaccc tgaataaatt taggactctg attcactgag caaaagcaga 1200
tgtgtcgagc atttctctac cccgttatgt attttgttag atttgtcaac aggaagcaca 1260
tgattcgaaa catcttggga cagaccaaaa ccaactgacg atggcaagcg tggcgagctc 1320
tgatttccct tctcaaatct cgcctaactc aaagatcttg agaaaactgt aaaaatttgc 1380
ctctgtcact caagttctac aaatgtttat ttgataaact cttaggtgaa ctatttccat 1440
gtctgtgata taggcatctt attcactgca cccgtgcaca cccagcacc cccgtccccc 1500
acattatttg aaagactggg aattcaatgg tcagggaacg taaactctat tctttttcca 1560
gggagcagctg tccctctaaa agttaaaagt aatacaagaa aactgtctat ttttagccta 1620
aagtaaaagg tttgaagaaa attcatttta cattgggtag acagtaaaaa acaagtaaaa 1680
taacttgaca tggagcacc tttagatccct cccctccatg ggctttggcg cacagaatga 1740
acctttgagc cctgtaaaagt ggattgtaat ttctataaag ctgtaaatgt ggaggtatgc 1800
tgggttccat tgaattgacc ctocaaaagt accattcaaa taacctggga gaatgcatac 1860
aattattcag ataaattaaa ctgcatgaat ctgattcaga ggcattgca ttacatttgt 1920
gcccttaata ccaatttgat atcataaata caagtgaatg caattggaat tttagtaaca 1980
aaccttaatt ttaaaaagg gttagacaaat gttggttaaaa aaaaaaaa aaacagttac 2040
aggttctctg tgtttgcacc aagtaattga catgtttttt gtttaataca tgtggaccat 2100
gaacagttat cacttacttt tttcaaatga tatgtgttag aaaaattctc tgaagaagt 2160
gagattttaa aatttttccc tttcaatgtt gttttaatgt tatttcttat tttgtttttt 2220
tgattgatag cacagtgtata aatcataata ctgacacaaa tctgtctctc tctcaacaaa 2280
gagccatata tatgtctgta tatatgggac ctactgcttc tctgaggaaa tgcataatct 2340
gttaatatca gacaaaatga gcaatttgga gtgtctataa tatattccaa ttttttttgg 2400
aattttcgat ggaattgtat ttcaataaag ccatgcaagg tgaaaacttt ataaactttt 2460
accttcaag tttaggtgaa ttctgatcca attttggta cttcccaatg tccccaatg 2520
caaatgctca aattacaatg cagacattaa gaaaagaagt tgactggagg ggttgaattc 2580

cttgagaatt tattttatag tctaaatcac aaatacttta ctcaatttag ttttaaaat 2640
agtaaaactga atatttttgt tgaagaacct caagagtcda ttctgttttt ggaattgttt 2700
tctgtttttt ccttactata aatcatttaa aaactgaaat cattttctta gatgctaaa 2760
gtctgtctct tgagaaaaaa gtaaaaactc cctattttca gtatctgtag caactgaaa 2820
aggcttttgt atagccagaa acaagttatg ttgaagttag cttttctttg tcaacagttt 2880
tgagcaacaaa aaactctgaa gtatttaaac ttgattttct actcgtggccc ttcaagctgt 2940
gtttggagaaa atttcaaccag ataatctaca tttagagtata atcatgtgtg atcagtaatt 3000
ggactaggtta atcaagattt gttgtcactt aaattttttt tgattttttt ccaagccagt 3060
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tacaactgtt ttttgcagct tataggcagg taaattttgc tattactatt gaatacaaaa 3180
gacaattctat ttatgcacc tcaaaacagc tttagtaaca ttttagtaca aaggtataaa 3240
acatccatct ggaattgtta tttgaagatg taaatttatc gtgttttaaa tttttccagg 3300
catctgaaaa ccttatctgc tagacaatgt aagattcaaa cagagtttat tgggattctg 3360
attttttaaa tagtacatat cattaaacca ttttctctaa atgtaaagag agcagaaaaa 3420
atctttataa attatcagat ttttctaatg acacagaaat gtaagaaaaa aatctcttta 3480
tattgaaaaa agatgcagtc aaagtctttt cagacatgac caaacctgga gaattctctt 3540
aacccattaa tgctataaag attttgttct ttctgtttca caaccagtgt tataacagaa 3600
ataactagct ctgtttttct tctgtgtgtg gaagtaatga atctgtattt atgtgactgt 3660
ttatgtattc aattaaacac taagaataaa aacatttcaat cctttaatta ataaaaaaa 3720
aaaaaataaa aaaaaaataa aaaaaaataa a

```

## (2) INFORMATION ON SEQ ID NO. 107:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 300 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

cgctcggccc ccgaggagag atcgaggtgt acttggccaa gactctggcg gaaaagctgt 60
atctatgtca gtacctgtgt cgtccagcct cgatgacctt cgatgacctt ccgcacctct120
cagccaagat caagcccaag cagcagaagg tagagcttga gatggccatt gacacctga180
accccaacta ttgcccgcagc aaaggggagc agattgcgct gaacgtggac ggggcctgcg240
ccgacgagac cagcacgtat tcctcgaagc tgatggacaa gcagaccttc tgctcttccc300

```

## (2) INFORMATION ON SEQ ID NO. 108:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1465 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

gccaaccttc cctcccccaa ccttgggggc gccccagggt tctgtggcac tgcctgttcc 60
tctctgggtgt cactggcagc cctgtccttc ctaggaggac tggaaacctaa tttctcctgag 120
gctgagggagg ggtggagggt ctcaaaggcaa cgcctggcccc acgacggagt gccaggagca 180
ctaacagctac ccttagcttg ctttccctct ccctcccttt tattttcaag ttccttttta 240
tttccctcttg cgtaacaaacc ttcttccctt ctgcaccact gcccgtaacc ttaccocgcc 300
cgccacctcc ttgctacccc actcttgaaa ccacagctgt tggcagggttc cccagctcat 360
gccagcctca tctcctttct tgcctagcccc caaaggccct ccaggcaaca tggggggccc 420
agtcagagag cgggcactct cagttgccct ctggttgagt tggggggcag ctctgggggc 480
cgtggcttgt gccatggctc tgcctgaccca acaaacagag ctgcagagcc tcaggagaga 540
ggtgagccgg ctgcaggggc caggaggccc ctcccagaat ggggaagggt atccctggca 600
gagtcctccc gagcagagtt ccgatgccct ggaagcctgg gagagtgggg agagatcccc 660
gaaaaggaga gcagtgctca cccaaaaaca gaagaagcag cactctgtcc tgcacctggt 720
tcccattaac gccacctcca aggatgactc cgatgtgaca gagggtgatg gccaaccagg 780
tcttaggcgt gggagaggcc tacaggccca aggatattgt gtccgaatcc aggatgctgg 840
agtttatctg ctgtatagcc aggtcctggt tcaagacgtg actttcacca tgggtcaggt 900
ggtgtctcga gaaggccaag gaaggcagga gactctattc cgatgtataa gaagtatgcc 960
ctcccaccgg gaccgggccc acaacagctg ctatagcgca ggtgtcttcc atttacacca 1020
aggggatatt ctgagtgtca taattccccc ggcaaggcgg aaacttaacc tctctccaca 1080
tggaaacctc ctgggggttg tgaaactgtg attgtgttat aaaaagtggc tcccagcttg 1140
gaagaccagg ggggtacat actggagaca gccaaagact gagtataata aggagagggg 1200
atgtgcagga acagaggcgt ctctcctgggt ttggctcccc gttcctcact tttccctttt 1260
cattcccaac ccctagactt tgatttttac gatattctgc tctctgtccc catggagctc 1320
cgaattcttg cgtgtgtgta gatgaggggc gggggacggg cgccaggcat tgttcagacc 1380
tggtcggggc ccactggaag catccagaac agcaccacca tctaacggcc gctcagggga 1440
agcaccggcg ggtttgggcg aagtc

```

## (2) INFORMATION ON SEQ ID NO. 109:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

cgggcggagg agcaggatgg agatccctgt gcctgtgcag ccgtcttggc tgcgcccgcg 60
ctcggccccc ttgcccggag ttctgggcgc cggacgcctc ttgaccagc gcttcggcga 120
ggggctgctg gaggccgagc tggtgcgctc ctgccccacc acgctcgccc cctactacct 180
gcgcgcaccc agcgtggcgc tgcctgtggc ccagggtgcc acggaccctg gccacttttc 240
ggtgctgcta gacgtgaagc acttctgcgc ggaggaaatt gctgtcaagg ttgtggggcg 300
acacgtggag gtgcacgcgc gccacgagga gcgccgggat gagcacggat tcgtcgccgc 360
cgagttccac cgtcgtacc gcctgcccgc tggcgtggat ccggctgccc tgacgtccgc 420
gctgtccccc gagggcgtcc tgtccatcca gccgcacca gcgtcgccc aggccccc 480
gccagccgca gccaaagtag agggggctgg gccgcgccc gcccccggga gccctccagc 540
gctccctcta ttaaaaggca tctgactccg ccagccaga tgtcccgagt gcgccaagga 600
ctgtcccttc acccactcct ggattctgcc ctgacctcca tcttggaac tgccctgata 660
acatagacc ttccactgac accctgcctc tcagagcccc tccagctttc cgaccccaca 720
ccgacaactc ccgggcttcc agaccctacc agcactacc taacctcag ccgacagtct 780
cagccccacc gaccacttt ctgtgcatat agccccactt aagaccctc ctctacttcc 840
ttctgagtc tctacaaaga catccgggta ctacatttcc atcccttccc tattttgaca 900
cgaattatg gtgtagacag ccttgcccca accccaggcc agtcaggcac aatcccccca 960
cccccaaac gtccctggact gccacagact cccactccag accatccagg cctggttccc 1020
aagaccgat ccttccctgc caaccagaca gtctacaact gcccccctca gcccattttc 1080
tgccgtgaaa ccccgagccg ccacaccaga ctctggaacc ctttttcgac tgcccacaact 1140
cttggaacc aggccaaacta gaacacccaa caccaaactg tacagactct cccaccgca 1200
cctccccaag cctctgcacg atgtcctagg cccctcccc aactcctaacc agaccccatc 1260
ccctaaagtc cctttgtctt gaaccccaag tcttcaacca gatctcctg gcaacccacc 1320
tcccaccctc cctctcttct ccttcaagac ccaactgagc acccgctctg attccccaca 1380
gcctttctcc ctgccaccac tcccttagtc ttctccaggc ttactctccc aataaatgtg 1440
ctagagctct gccaaaaaaa agaaaaaaa gtcgacgcgg ccggaatt 1488

```

## (2) INFORMATION ON SEQ ID NO. 110:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 783 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

aacatatgtt tgaagggtaa tttgagagaa atatgaagaa ctgaggagga aaaaaaaaaa 60
aaagaaaaa accaacaacc tcaactgcct actccaaaat gttgggtcatt ttatgttaag120
ggaagaattc cagggtatgg ccatggagtg tacaagtatg tgggcagatt ttcagcaaac180
tcttttccca ctgtttaagg agttagtggg ttactgccat tcaactcata atccagtagg240
atccagtgat cottacaagt tagaaaaacat aatcttctgc cttctcatga tccaaactaa300
gccttactct tcttgaaatt ttaacctatg atattttctg tgcctgaata tttgttatgt360
agataacaag accctcagtg cttcctgttt ttacacatttt ccttttcaaa taggggtctaa420
ctcagcaact cgcttttaggt cagcagcctc cctgaagacc aaaattagaa tatccatgac480
ctagttttcc atgcgtgttt ctgactctga gctacagagt ctggtgaagc tcaactctgg540
gcttcatctg gcaacatctt tatccgtagt ggggtatggt gacactagcc caatgaaatg600
aattaaagtg gaccatagg gctgagctct ctgtgggctg gcagtcctgg aagccagctt660
tccctgcctc tcatcaactg aatgaggtca gcattgtctat tcagcttctg ttatttttca720
agaataatca cgctttcctg aatccaaact aatccatcac cggggggtgg ttttaagtgg780
gct

```

783

## (2) INFORMATION ON SEQ ID NO. 111:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1045 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

tctgttctgt ggacaactgt tactgttctt ccgtggccaa ccattggcgc caccagccct 60
accocccgtc cggccacttt cctggacag tgccctcgca ggagtactca caccogctcc 120
cgccacacac ctcctgtccc cagtcccttc ccagcctggc ggtcagagac tggcctgacg 180
cctcccagca gcccgggccac caggatttct acagggtgta tgggcagccg tccacccaaac 240

```

```

actacgtgac gagctaacgc cagcgaggcg gcgggcgctt ggggaatctt cctccccagc 300
ccccgggctc gggagttatg catccagaga cctggccctc taccttcttc gccctcccc 360
ttcctcatto cattgccccga ggtcttttcc ttttggtatt tgttttgggt ttggctttgt 420
ttttgatttt tttttattat gaattctctg gacgcagagg tgacagtggg agctggcctg 480
ggccaggagc ggcaggtggcc ctggagatgg gaaagtgtct gtgtcgaggc gctgagctct 540
ctctctgttt ctctcttttt cctctactcc ttccccttca cccccccgtg gctggaagga 600
acctcggtct cctgaaaagc ttgggggtcc cacccttctt accccacccg ggaggaaagc 660
ccaggggccc gggctgtttt ctctctttgt tttcttttgg ggcagtttga tcaactgatc 720
agtaaggaat gaccttttaga ttgtgcgact ttgtgttttg ttttttttaa tttttttaaa 780
ccaagaatga tttctctgc ttctctctcc tcaccatctt cccagacagga gttcaaaagg 840
cactttctca gacgtctttg gcaaccttca cctcagagtg gaattcttta aagacaggag 900
ccctatgtcc aggaagaggg aaaaggaact ttgccaatga tagtgaccac agcaaaagca 960
aataataata atattataaa taataaaaag gaaaaaaaat aatagaataa aaacccaatal 1020
gcacagcccc ttgttggaag tccag                                     1045

```

## (2) INFORMATION ON SEQ ID NO. 112:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1386 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

cacactcact gcccatgaag gaagaggggg caagtgtacc gaggaagggg atgcctcaca 60
gcaagagggc tgcaccttag gttctgacct catctgcctc agtgagagcc aggtttctga 120
ggaacaagaa gagatggggg ggcacagcag cgcggcccca gccacggcca gtgtgaatgc 180
agaggagatc aaggtagccc gtattcatga gtgtcagttg gtgggtggag atgtcccaaa 240
ccgggatgtc ctgtctgcac acaagatga cgtgaaggag gagaagggtg gtcagggaag 300
tttcccagag ctgcccctca aggagtgaaa gggacaattt ggctgaagtc tttctctgaa 360
aaaagccaaa ggggttatagg ggtacactta ggggttgcat gcaagctgtt accaaaaaat 420
ttttaagtat tttcttaatt tgaataataa aaccagagga aatgcataca gggcatgagc 480
aacctgagga aaccttttgt gacatgaatt gttctacgat gaatttttgc tttagtattt 540
taataaagat tacaagaaca atggcctact tggggtgaga gggagctgag gatgtctgag 600
gagggaatat tattgcaggg aagactgaga aaacagtagg atgacagttt tgagtatact 660
ctgcactttt caatttgtga atcttcttgt gcacttttag gctttttaat tttgtttgag 720
aatgcaaatg tatactgtaa gtctactctt actatctact atgcccactt caccatctct 780
taaggactcg gcaattgtcc acagtacagc tgcagaagag ggtaggtctat gaacagtcac 840
ccgtgtctgc tgtagccccc acagaggcaa tcacgcccac tagattccaag agaagctaa 900
cggaatatga ggggtggaag tgtgatctgt gggactgtct gggctgttta ctcatctgc 960
tatcaatttc ttattaatca atcttgatga ttcttattaa ttaatcacat ttgcaggaaal 1020

```

```

ttcagatgag gcaagaaaaa ttatttggcc tgggttaagc tgaagaagcatt ccaaatagg1080
cttagactgt gcaaggggct tagctaagtt atcgagctta aaacccgcta attaaacaa1140
cattatttga acagttaact catgccacgc actgtgttgg gcttagtaat aaaaaaaag1200
aaagataaag gctttgtcta gcataaata aaaggctccaa ggaattttaa tctggaagag1260
aacatatgcc aattttttaa ctatgcacgc tttttttttt tttttccatt caaataggcc1320
cgggttcagc cccagaaggg cacaaaatga atgaataaat aaataaatga ataaagacaa1380
aaaaaa                                     1386

```

## (2) INFORMATION ON SEQ ID NO. 113:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1747 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

ccagtcctgtg agcccttgtc ctgtgggtcc ccacogtctg tcgccaatgc agtggcaact 60
ggagaggcac acacctatga aagtgaagtg aaactcagat gtctggaagg ttatacgaag 120
gatacagata cagatacatt cacctgtcag aaagatggtc gctgggtccc tgagagaatc 180
tcctgcagtc ctaaaaaatg tcctctcccg gaaaaacata cacatatact tgttcatggg 240
gacgatttca gtgtgaatag gcaagtttct gtgtcatgtg cagaagggta tacctttgag 300
ggagttaaca tatcagtagt tcagcttgat ggaacctggg agccaccatt ctccgatgaa 360
tccttgacgc cagtttcttg tgggaaacct gaaagtccag aacatggatt tgtggttggc 420
agtaaatata cctttgaaag cacaattatt tatcagtggt agccttgcta tgaactagag 480
gggaacaggg aacgtgtctg ccaggagaac agacagtgga gtggaggggg ggcaatatgc 540
aaagagacca ggtgtgaaac tccacttgaa tttctcaatg ggaaagctga cattgaaaac 600
aggacgactg gacccaacgt ggtatatctc tgcaacagag gctacagtc tgaaggggca 660
ctcagggacc actgcacaga aaatggaacc tggagccacc cagtccctct ctgcaaaacca 720
aatccatgcc ctgttccctt tgtgattccc gagaatgctc tgctgtctga aaaggagttt 780
tatgttgatc agaatgtgtc catcaaatgt agggagggtt ttctgtctga gggccacggc 840
atcattacct gcaaccccca cgagacgtgg acacagacaa gcgccaaatg tgaaaaaatc 900
tcattgtgtc caccagctca cgtagaaaaa gcaattgtct gaggcgtaac ttatcaatat 960
ggagactatg tcacctactc atgttacagt ggatacatgt tggagggttt cctgagggagt 1020
gtttgtttag aaaaatggaac atggacatca cctcctattt gcagagctgt ctgtcgattt 1080
ccatgtcaga atggggggat ctgccaaacg ccaaatgctt gttcctgtcc agagggctgg 1140
gtggggcgcc tctgtgaaga accaatctgc attcttccct gtctgaaacg aggtcgctgt 1200
gtggccctct accagtggtg ctgcccgcc tggctggacg ggtctcgctg tcatacagct 1260
gtttgcaggt ctccctgctt aaatggtgga aaatgtgtga gaccaaaccc atgtcactgt 1320
ctttcttctt ggacgggaca taactgttcc agggaaaagg ggaactgggt ttaaccactg 1380
cacgaccact cggctctccc aaaagcagga tcaatctctc tcggtagtgc ctgggcatac 1440
tggaacttat gcaaaagaaq tccaacatgg tgcgtgggtc tgcttagtaa acttgttact 1500

tggggttaac ttttttat tggatata tttgttatt cttgtgacat actttcttac 1560
attgtttccat ttttaaatat gctgttatt tctatataa aatatattat aatagatgct 1620
gcttaccctt cacaataatt acatattctg ctgtctattg ggaagttcc ttgtaacacat 1680
ttttattcag ttacttaaaa tgatttttcc attaaagtat attttgctac taaataaaaa 1740
aaacgcg

```

1747

## (2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1526 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

cgagccca  ggccccggag  tagcagcggg  gaggcgggga  gcccgcgggc  cggagccggc  60
cggcgcaggc  gtgggggctg  cgggggccgc  ccatccgtgg  gggcgacttg  agcgttgagg  120
gcgcgcgggg  aggcgagcca  ccatgttcag  ccagcagcag  cagcagcagc  tccagcaaca  180
gcagcagcag  ctccagcagt  tacagcagca  gcagctccag  cagcagcaat  tgcagcagca  240
gcagttactg  cagctccagc  agctgctcca  gcagtcacca  ccacaggccc  gttgccatgg  300
tgtcagcggg  ggtccccccg  agcagccaca  gcagccgctt  ctgaatctcc  agggcaccaa  360
ctcagcctcc  ctccctcaacg  gctccatgag  gcagagagct  ttgcttttac  agcagttgca  420
aggactggac  cagttttgaa  tgcccaccag  caoctatgac  actgccggtc  tcaccatgcc  480
cacagcaaca  ctgggttaacc  tccgaggcta  tggcatggca  tccccaggcc  tcgcagcccc  540
cagcctca  cccccacaa  tggccactcc  aaatttgcaa  cagttcttcc  cccaggccac  600
tcgcagctcc  ttgctgggac  ctccctctgt  tggggctccc  atgaaccttc  cccagttcaa  660
cttttcagga  cggaaacccc  agaaacaggc  ccggaacctc  tcctctacca  cccccaatcg  720
aaaggattct  tcttctcaga  caatgcctgt  ggaagacaag  tcagaccccc  cagaggggct  780
tgaggaaagg  gcagagcccc  ggatggacac  accagaagac  caagatttac  cgccctgccc  840
agaggacatc  gccaaaggaa  aacgcactcc  agcacctgag  cctgagcctt  gtgaggcgct  900
cgagctgcc  gcaaaagagat  tgaggagctc  agaagagccc  acagagaagg  aacctccagg  960
gcagttacag  gtgaaggccc  agccgcaagg  cggatgacag  taccgaaaca  gacacagaca  1020
ccagacctgc  tgcttgaggc  cctggaagcc  actcagccgc  ggataccatc  gccacgggtc  1080
ctgcaggtcc  aggccccagg  gcatcacaag  caaacacaga  cctctccaga  gcacttagtg  1140
ctgcaacaga  agcaggtgca  gccacagctg  cagcaggagg  cagagccaca  gaagcaggtg  1200
cagccacagg  tacagccaca  gccacattca  cagggcccaa  ggcaggtgca  gctgcagcag  1260
gaggcagagc  cgctgaagca  ggtgcagcca  caggtgcagc  cccaggcaca  tttcacagcc  1320
ccaggggagc  gtgcagctgc  agctgaggaa  gcaggtccag  acacagactt  ttccacaggt  1380
gcacacacag  ggcacagcca  agcttccagg  cacagggagc  ttcttccggg  cgcggtgttc  1440
agtttcaggc  caccaggggc  agggcc

```

1526



## (2) INFORMATION ON SEQ ID NO. 115:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1205 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

cccgagaaaa accaatTTaa tgcttctgtt ctcagcattt cacagcatgc aggactcaaa 60
tggatacaac agaagaaaaa aaccocaaat ttttggaaaa ccctttgttc aatgattcat 120
attttgatat ctattgacaa tcccttagaa ctttaaattc caaaaacaaa aaagtactgt 180
ggatctccct cgagccgaat tcggctcgag ggcggtcacc tggagatgag aaaggcccg 240
gggggggacc atgtgcctgt gtccacagag cagccgagag gcggggagga cgctgctgcc 300
caggagccca ggagagggcc agagccagag ctgggggtca aacgagctgt cccggggggc 360
cagaggccgg acaatgccaa gcccacccgg gacctgaac tgagggtggt ctcogacctc 420
cggaggcgac ggagggaact tggccctcat gcagagggtc agctggcccc gagggatggg 480
gtcatcattg gccttaaccc cctgcctgat gtccagggtg acgacctccg tggcgccctg 540
gatgcccgcc tccgccaggc tgcgggggga gctctgcagg tggccacag ccggcgagctt 600
agacaggcgc ctggggctcc agaggagtcc tagcacctgc tggccatgag gggccagcca 660
gccactgccc tccctggcca gcagcaggtc tgtctcagcc gcatccagc caaactctgg 720
aggtcacact cgctctcccc cagggtttca tgtctgaggg cctcaccagg tgtgagtgc 780
agtataaaag attcactgtg gcactcgttc cagaatgttc ttgctgtcgt tctgttgtag 840
ctcttagtct gaggtcctct gacctctaga ctctgagctc actccagcct gtgaggagaa 900
acggcctccg ctgcgagctg gctgggtcac tcccaggctc aggcctgggga gctgctgcgt 960
ctgtggtcag gccctcctgct cctggcaggg agcacgcgtg gtcttcgggt tgagctcggl020
cgtgcgttga ggtgcgcagt gctgctcatg gtcccaacac aggcctactgt gagagccagc1080
atcccaacccc acgcttgtag tgaactagaa tgataattat tatgactgtt tatcgatgct1140
tcccacagtg tggtagaaag tcttgaataa acacttttgc ctttcaaaaa aaaaaaaaaa1200
aaaaa 1205

```

## (2) INFORMATION ON SEQ ID NO. 116:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3968 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

ggatatttcta aaacataaag aggagaatta agtcagctgc agaacaatagg ggctgattct 60
tctgctttttt cctcggaaaaa tctttcattg cttttgggtgg aaatttacct agagggttaca 120
accacaggat gtacgttgggt cctctattttg cctttttggg aaaccaatta agattaatac 180
aggataaagg aaaaagcaaa tctatttcatt atataacaca gttgttttga ttaactgttc 240
cctgcaaaag aaatctgttg aatgcttgca ttttgaaatc ttttctaata gaacaaacca 300
aaaaggcttc tcatggtgca gcaggaaaaa agatcatttt tatagctttg cttctctaac 360
atagcattta aagagcggca tgaatttagag gaaagacatg gaacacacag gtatgcggtt 420
tgagatcatc ggcttaaaag tatcctagga tggtaatgac ccagaagtat ttccagttgt 480
ctagtgtgtt ggtatgcagg aatgagaagt gttttcttcc catttccctgt tggacaggtg 540
gcaatcttag cagagccact atttggagtt gataactaaa gatgcaaaata acatgactat 600
gcctctctggt catcctagga ctatttggag ttctccaaaa ccttgtaaga ggcgatgtcag 660
gcatgcagta aaagcatcta caacttcagc tgggcactgg cagcataggt ctcactcttg 720
accatcacgt ccacttttat agaagaggggt ggaagtcttc caaaacaata tccacaacaa 780
agcttgacct cactctgagg gagatgggaa gtggggaggaa gaaggactaa ccagctccct 840
ggagttaagag gaatttgcct tccctgtctg cccaccaggg gctatatgtg ccaccttcca 900
ggttggggccc aaggaaagtga tgtcagttgt acagaaggga gagttagacc tccagacgtc 960
agcctccctc ccattggggtta cattttcaat ctgagtgttg ttgccttagc tgtgttggtal1020
ttagcttgat tgggttggtcc gctggttatg aggtgtaggg aggcagtttt tgttttagtt1080
ttagagacttt gcctcttccct ttgtccttag cataatttct aggcagagca tgcgttggtal1140
cggttttcat tgccagctca agagcgacaa tcaatttacga gttcctatgt tatgttaggt1200
gccttatgta tattatccca aatccactgc atggtttaaa tacaggcact ggaatataaal1260
tgaaaaaagg cattacagtc actgactttc tgcaggacct taacactttc tctttccacal1320
agtttccctc taatcatgtg tcaaacctct cttcctgagc ggaatgttgt gctataatgal1380
atctgcataa cgccttgggat tctaggagga aggaaggttc catggacatg taagtacagc1440
atattccctc cagctttcta ggagggcaga gtgaatccca gaactggtaa gattgggaat1500
ctgagcattt ccactttaat cttagaatat ttatcatttt gacacatcct gttttttaga1560
gaggaaaaa aacacagttt ctgcatttgt agtgtaaaag ataccttgtt aggaacgtgt1620
tttgttaagc acatttgggt ttgtcattcta gagcatgtca aactttgtac ttcaaaatat1680
atttagtatg attgttagtg gtaacatata tcaaggcttt gaattaaactg ttttatttaa1740
ttttcacagg aagcacttat tttagccata ggaaaaccaa tctgagctac aaatagttct1800
ttaaaaataag cccaggttat tttagctattc tagaaagtgc cgaactcttt ctgacctggc agcaagagtc1920
gcattttagg acagctgaga attatcacat agcctaaaatt ctgacctggc aagggggtag1980
acatctgaga tgtccaaaaa aaaaaaaa aaacacctga tctacattga aagggggtag2040
actaacgtat gtgagacct tttcctattt gcagttacaa ggttaaaagaa ctttgaaggt2100
cattcggctg ctaagaggca tctcgaacac tctgtgtggc tctttccacag taacacctcc2160
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ccaacactgt attcccgaaa acatgacctc cgtggtctt gggtccacat atcaattggac2580
tctggggggac acaaaagatgc ctgtgacct tgggtgttgc cgagttagtc aacaattatt2640

```

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ctgggaaaaa gcagaattga attctctctc agatgtccta ccagggttgg ccaagggcca2640
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atgagcgtca tgcgaatgaa accccatctt ctggagaagc ccttgatca gaattatctt2820
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taatttttct aattttttatt ttttggttcc aaatgtaaag ctccctgtgt ttacctctgt3180
ttatgtcatt cttgacatgt ttatcctaat tatgtgtgct ctgtgacagg tgaaatgtaa3240
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tacctgataa tgataatact caaataaaca acattcaaa gaaacacaaa gaaatcctgc3360
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aatttttaaa tcaaaagatt gtacttggcc ctgagttgaa aaaatttcaa aaatcaaaaag3480
tttgactctg gcctctgatt gaaaaaaaaa attcacattc taagaataaa cagaaaaatg3540
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tttctactat atgcaggaaac tgtgttaaat attttacata agttttgata atagctaaca3840
ttagctgaga accaaaattg ggccttgatt tgtgctgagt atctttcaca gattactgct3900
tttaatcagc agtccttggt agctagggat gatcattatc occatttata gattacggat3960
gagattcg
3968

```

(2) INFORMATION ON SEQ ID NO. 117:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 798 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

gtaatgggaa atttggtgtg ctgaatcttc ttctaggat attgatatat tccacgcttc 60
taqtgggtrt tctgggaatt ttacctgct cagtattttg cctagggtac tagaagagg120
agattgtcca aacttagcag tatggtccat ctggtgtaga agtggaagtg tcatacaggal80
tagcaaacac tcttgggttc tttttgccc ggccttgccc gagccggcaa cagcaacaaa240
atgtggagga tgcaatgaaa gagatgcaaa agcctctggc ccgctatat gatgacgaag300
atctggatag gatgctaaga gaacaggaaa gagaggggga cctatggccc aacttcatac360
agaagaataa ggccaaggag aacaagaata aaaaagttag acctcgctac agtggtccag420
cacctccctc caacagattt aatatctggc ctggatatcg ctgggacgga gtggacagat480

ccaatggatt tgaacagaag cgctttgcca ggcttgccag caaagaagcca gtggaggaa540
ttgcctacaa atggagtggt gaggatatgt aactttctct aggcctgtgg ggtggctggg600
ctgtggtagt gggcataggc agcgagatat ccagtgttaa cagtgtgtct tgcttaaat660
tgagagccac acagaccagc aacttgttga atgccagtt tgaccacaga agaattattc720
agacctgatg tttggattga ggtacctgta cttcttgggg tgttgacagc agcgggtgtt780
ggtgggtttt cagaggaa                               798

```

## (2) INFORMATION ON SEQ ID NO. 118:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1068 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```

ccctctctg tgactcagtc tctgagcgtt ttaatacagat ggtgtccccc cgggatcaaa 60
cttcagcgctc acagctgagg actggctctg tggctccctga tgggagagca tgaacaggtg 120
gtatgtgaag cccttgggaa ccagctcttc caaagtcaaa gccaaagacca ttgtgatgat 180
tcccgaactcc cagaagctcc tgcgatgtga acttgagtca ctcaagagcc agttacaggc 240
ccagaccaggc gctttcgagt tcttgaacca ctacgtgacc atgtttggaga aggagagctg 300
cttgacagcaa atcaagattc agcagcttga agaggtgctg agccccacag gcccgccagg 360
agagaaggag gagcacaagt ggggcatgga gcaggggccg caggagctgt atggggccct 420
gacccaaggc cttcaggggc tggagaagac cctgcgtgac agtgaggaga tgcagcgggc 480
ccgcaccact cgctgcctgc agctgctggc ccaggagatc cgggacagca agaagtctct 540
gtgggaggag ctggaactgg tgcgggagga ggtgaacctc atctatcaga agctccaagc 600
gcaggaggat gagatctcag agaacttggg gaacattcag aaaaatgcaga aaacgcaggt 660
gaaatgcgcg aaaaactcga ccaagatgaa gcagcagggt catgagacag ccgctgtctc 720
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ctgagtgtata tatgttctgc tgtgcacgtg ctgcagaact ccatagacag cctcactctg 840
tcttcggggg cctgtcccaa ggcctcgagc ctaagaggcc acaaggggca ccatgtcctg 900
agccctccac tccctctctg ggactctgac tccagactctg accagagact ctcccagca 960
cctttcagca agagcggccc ccccttccca ccgcttgag cagccgggag tgctctccct1020
gaagaccctc ccagagagaa aataaaactg ccagaccct cctctaaa 1068

```

## (2) INFORMATION ON SEQ ID NO. 119:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 4584 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

ctcgagccgc tcgagccgcg gaagtaattc aagatcaaga gtaattacca acttaattgtt 60
tttgcattgg actttgagct aagattattt tttaaatcct gaggactagc attaattgtac 120
agctgaccca ggtgctacac agaagtgatc tcagtgaatc taggaagaca gcagcagaca 180
ggattccagg aaccagtggt tcgatgaagct agggcttggg gcaagagggc aagcagcagt 240
tggttggtgaa gataggaaaa gagtccagga gccagtcgca tttggtgaag gaagctagga 300
agaaggaaag agcgctaaag atttggtggt gaaaagagga attgggagtg gtaggatgaa 360
acaattttga gaagatagaa gtttgaaagt gaaaacttga agacagaagt acggggaagcg 420
gaagaaaaa gaatagaaaga tagggaaatt agaagataaa aacatacttt tagaagaaaa 480
aagataaatt taacactgaa aagtaggaag cagaagaaaa aagacaagctt aggaacacaa 540
aagctaaggg caaatgtac aaacttagaa gaaaatttga agatagaaac aagatagaaa 600
atgaaaatat ttcgaagagt ttcagataga aatatgaaaa caagctaaga caagtattgg 660
agaagtataa aagatagaaa aatataaagc caaaaattgg ataaaaatgc actgaaaaaa 720
tgaggaaaatt attggtaaac aatttatatt aaaaagccat caatttaatt tctggttggtg 780
cagaagttag aaggtaaagc ttgagaagat gagggtgttt acgtagacca gaaccaattt 840
agaagaatac ttgaagctag aagggggaag tggttaaaaa tcacatcaaa aagctactaa 900
aaggactggg gtaatttaaa aaaaactaa gcaagaagct tttgggaagag ttagaagaa 960
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gtaattcaag atcaagagta attaccaact taatgttttt gcatgtgaact ttgagttaa91080
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gagggtgggg gagaaaatgt tttttcttaa gattttccac agatgctata gtactattga2340

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caaaactgggt tagagaagga gtgtaccgct gtgctgttgg caccgaaccc ttcaggggact2400
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cctcttagag aggtggggaga ttatgatcag agtaaaaggt aattacacat ttattttcca4440
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gaccttatat agggaaaaa tga

```

## (2) INFORMATION ON SEQ ID NO. 120:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 982 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```
gtggaggggga cctctgtggtt agcagcagct atcgacagct cggatgttca gagcagcaga 60
agcggcgctgc gtctgattgtt gtgttgcccg ccaccatgag ctacacaggc tttgtccagg120
gactctgaac cactttgcag tcgacatact cggataccag cgctcagccc acctgtgatt180
atggatattgg aacttgggaac tctgggacaa atagaggcta cgagggctat ggctatggct240
atggctattgg ccaggataac accaccaact atgggtatgg tatggccact tcacactctt300
gggaaatgcc tagctctgac acaaatgcaa acactagtgc ctctgggtagc gccagtccc360
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tgatgcaagg aggcgtgtac ggctcaggtg gagaaggta tgactcttat gagtccctgcg480
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gcctcgctgg caacgacacc ttctgtccca gggcacaggc ctggggcccg gatgcccgga660
gcggccggcc aatggccgca ggctatgggc gcattgtgga agaccccatg gggggccggg720
gccagtgcct gtctgtgtgcc tctcggttgc cctccctct tctccagaa catcatcccc780
gagtagcgca tgttccaggg gcattcgagg ttggggcgcc tcccgggcg gcttccgctt840
ttggttttcg ggttttgcaa tggcatgaag cagatgaggg cggactggga agacggggac900
cacagccgat ttgcgaacca agaagaagaa gaaaaagcag ggcggcattc tgattgagcc960
agttagcaaa gcagccggaa tt 982
```

(2) INFORMATION ON SEQ ID NO. 121:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 742 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```

ctcaacttcg  cagcactcgc  tgcctcaagc  cgacgcagcg  gcctactctc  gcactgcaga  60
cggggaaact  gagggccgag  gcggccgggg  tggggcagac  ctcccggcga  gcccgagccc  120
ccgcccccg  ctgccccgc  cctggcccg  aagaagcacc  cggggcgcca  ggcgaagcgc  180
cacagcgcg  ggccagcgt  ggtccagcag  cgcgatggca  gctcagcgcc  tgggcaagcg  240
cgtgctgagc  aagctgcagt  ctccatcgcg  ggcccgcggg  ccagggggca  gtcccggggg  300
gctgcagaag  cggcacgcgc  gcgtcacogt  caagtatgac  cggcggggag  tgcagcggcg  360
gctggagcgt  gagaagtgg  tcgacgggg  cctggaggag  ctgtaccgcg  gcatggaggc  420
agacatgccc  gatgagatca  acattgatga  attgttggag  ttagagagtg  aagaggagag  480
aagcgggaaa  atccagggac  tcctgaagtc  atgtgggaaa  cctgtcgagg  acttcaccca  540
ggagctgctg  gcaaaccttc  aaggccctca  caggcagccc  gccctccgcc  agccaagccc  600
ctccccgac  ggcagcctca  gccccctcca  ggacggggcc  cggactgctc  acccctgacc  660
ctcttgact  ctccctgcc  cccggacgcc  gccagcttg  cttgtgtata  agttgtattt  720
aatgggtctg  taacaataaa  aa

```

742

## (2) INFORMATION ON SEQ ID NO. 122:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2330 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

gtttggaacaa gttgttttaa taggaatatg acctgcgtgc ttcataggtt tctcaacca 60  
 cctttcctca gctttcttaa aatgggatct acattgctgc ttcaacacca aatagcagac 120  
 taactgcttt tctgcttagc accgtctggg tcaattgtct gaactctgcc ttacagcagc 180  
 aagaaaaatt tctcgaccaa gaacctcaat cttagtcc attgagctcc cctctcggt 240  
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 aggtctgaag aggagactac caaagcagtg ttacaaacc cagagctcac acaacctat 360  
 tgcatagaac agcacttgcc ttccacaagc ctctacagc acctggtgta attggagtga 420  
 aagggcagag accctggagc tggaggtggc tggtgtctgc gatgggaaga aggcagaagg 480  
 cccaggggct ttggacatag agcaggggtg aagctgcaag tactgggaag gaagagagtt 540  
 tcacagaaac aaagctttgt cacacagaaa tgagttctgt ctcactgggt acctcatccc 600  
 tcaggctcca gctgagcaga gattttaatc agcttcttta atgggtattg acactgctca 660  
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 aatagatcaa ctctattgta gtccaggaac tggttggtcac agctactagg aatgaggtga 780  
 tttctgaggg ctgagaaaaa acacagaatc ttggccagca gccagcagct cccaggtgaa 840  
 agatgcattc actttctcct tgagagttgg ggttgagggc aaacatagaa ccacaggttg 900  
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 tttaaaaatg ggtctggcat atacttgatt acaaatgaaa actcagaaac caattttatt 1140  
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 gctgtttccc aattctatctg ctatttttgg accatgaatc tgccaagagtg atattttctg 1260  
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 taagggtgac tcaggatgct cttatgtcct tccagaataa gcatacact cactctctct 1380  
 cctttcactc cctctgcat tcttaattcc ttgctttctt cacttgggagc cgaggggtgt 1440  
 tttagagaggt ggttttccat gaatcagcca agatttctgt agaagtggg tacacctatt 1500  
 ccagcttcaa agctctccgg ctatgctaatt gtccccctag agatgaggtt tgacttttag 1560  
 gcccgtatga ctctccata gcttgcccaa ggagaccatg agtagccatg tctggtttac 1620  
 tctttatcct gagactgttt gtttatagct taaaaacagaa gtgtgtcttc ccagcacaaa 1680  
 cctaatacat cagtgtatca gtgcatctgg tggcaacagc tcagccatt caaagacaa 1740  
 ggattcagga aaggcacact gatgggtggg agctcttaa gagcctctaa tgttctccaa 1800  
 aaacacagat tgagagtgg agtgccagt gtcggggccc actattcctg aataaggga 1860  
 atgcaagggt cagaagtgc ttgactctcg cctaaatctc tgtgcttttg cctgtcctt 1920  
 ctcccactct actgaaccc ggaacagatt cccgcttgcc ttctgatgaa gagaggttag 1980  
 gtaaaagagag tttggaggaa aaaagacacc aggagcgagg ctgtggggta ggagaggtt 2040  
 ctgagagggg gcagcaatcc agaatacctc cttttctagc cagcatcctt tgaacttttg 2100  
 aaaggtctgt gctaccactg cctggcacac cagggcaatg attccccgc agaagggaag 2160  
 aaagaatggt ttcaccttg catccttctt gggagaagct accagcctgt tgcctcagtt 2220  
 tgagttgggt tcacattcag gattttgggg ttttctgggt ttctctctct cctctgtgtt 2280  
 tgccccgaac gtgtatcaac aggggtgaaa aagggccacc tgagggtttc 2330

## (2) INFORMATION ON SEQ ID NO. 123:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1860 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

gaggcagttt gagatcacca gcatttcctg ggatgtctgg cacatcctgg aattcgacta 60
tagcaggctc cccaaacaaa gcctcgggca gttccatgag ggggatgcct atgtgggtcaa 120
gtggaagtcc atggttgagca cggcagtggt aagtcgccag aagggaagagc actcgggtgag 180
ggcagccggc aaagagaagt gcgtctactt cttctggcaa ggccggcact ccaccctgag 240
tgagaagggc acgtcggcgc tgatgacggt ggagctggac gaggaaaggg gggcccaggt 300
ccaggtttcc cagggaaagg agccccctgt tttcctgcag tgtttccagg ggggagtgtg 360
ggtgcactcg gggaggcggg aagaggaaga agaaaatgtg caaagtgagt ggcggctgta 420
ctgcgtcggt ggagaggtgc ccgtggaagg gaatttctgt gaagtggcct gtcactgtag 480
cagcctgagg tccagaactt ccatggtggt gcttaacgtc aacaaggccc tcacttacct 540
gtggcacgga tgcaagccc aggccccacac gaaggaggtc ggaaggaccg ctgcgaacaa 600
gatcaaggaa caatgtcccc tggaagcagg actgcatagt agcagcaaaq tcacaataca 660
cgagtgtgat gaaggctcgg agccactcgg attctgggat gccttaggaa ggagagacag 720
gaaagcctac gattgcattc ttcaagatcc tggaaagttt aacttcggcg cccgctgtt 780
cactctcaag agctcctctg gggattttgc agccacagag tttgtgtacc ctgcccgagc 840
ccctctctgt gtcagttcca tgcccttctt gcaggaaagt ctgtacacgg cgccccagcc 900
agcacttttc cttgttgaca atcaccacga ggtgtacctc tggcaaggct ggtggcccat 960
cgagaacaaq atcactggtt ccgcccgcac ccgctggggc tccgaccgga agagtgcgat 1020
ggagactctg ctccagttac gcaaaaggaa aaatctcaag aaaccagccc ccaagtctta 1080

ccttatccac gctgggtctg agccccctgac attcaccaat atgtttccca gctgggagcall140
cagagaggac atcgtctgaga tcacagagat ggacacggaa gtttccaatc agatcacct1200
cgtggaagac gctcttagcca agctcctgtaa aaccatttac tcgtctggccg acctcctggc1260
caggccactc ccggagggggt gcgtcctctg aagcttgaga tctatctcac cgacgaagac1320
ttcagatttg cactagacat gacgagggat gaatacaacg ccttgcccgc ctgggaagcag1380
gtgcaacctga agaaagcaaaa agccctgttc tgagtgggga gacgccagag gacgctcaag1440
gtcacgtcca acaacaccac tgcaaccagg aaatggatat atatttttgg actggtgttt1500
ttcacaaaat atttttcaat cacagttttc agaacctgac attgttaaaq atactgcttg1560
tcccgagatt ggtgtatttg taaatgttca agggaactgt ttggaaaact ctttccacca1620
ttcaggaggt tatcagaagt aataaaaagta tctgttatgt gcaacttaagc cgcagctgct1680
atagatagca ctgccttctt gttccagcta ggcaatgcct tttttttttt tttagaacag1740
ttctctttat aaagtgttat ttgatagtt tgtggattct aaatacccat ataagtcaaa1800
tatggattta acaagcaaat atgtattcat tcaatttcca gatttggggg gttgtttttt1860

```

## (2) INFORMATION ON SEQ ID NO. 124:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 807 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

cctttctctca tctctattaa attgtaaaca ggactactgc atgtactctc tttgaggtga 60
atttggaatg gaaggccagg gactatactc tttttaaaat agacatttgt ggggctcaca120
caatatatga aatagtagcc tctaaaaaag agaaaaaaa aatcaggcgg tcacacttag180
agcaacattg tcttattaaa gcatagttta tttcactaga aaaaatttaa tatcaaggac240
tattacatac ttcattacta ggaagtctct tttaaaaatga cacttaaaac aatcactgaa300
aacttgatcc acatcacacc ctgtttattt tcottaaaca tcttggaaag ctaagcttct360
gagaatcatg tggcaagtgt gatgggcagt aaaataccag agaagatgtt tagtagcaat420
taaaggctgt ttgcacctt aaggaccagc tgggctgtag tgattcctgg ggccagagt480
gcattatggt tttacaaaa aatgacatat gtcacatggt tgcattgttg tttgctgttt540
gaatttttga acagccaggt gaccaatcat agaaagtatt accttctttt atatggttt600
tgggttcactg gcttaagagg tttctcagaa tatctatggc cacagcagca taccaggttt660
ccatcctaag agggaaatgga aattaatttt gtaacctact gattaacaga atctgggggt720
cacattggaa aaaaattctt ttatcgtct ttaaggata tgtttaataa ttattttatg780
tgtcggcata ttgcggcacg tctgaga                                     807

```

## (2) INFORMATION ON SEQ ID NO. 125:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1932 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

ccgggggtttt gggctggaac tgcagcgctt agagagctcg gtggaagctg ctaaaggcgg 60
aggcgggggct ctggcgagtt ctctctccac ctccccccac ccttctctgc caacgcgtgt 120
ttcagccctt agctggattc cagccattgc tgcagctgct ccacagccct tttcaggacc 180
caacaacccg cagcgcgtgt tcccaggatg gtgatccgtg tatatttgc atcttccctt 240
ggctctcacg cgattaagaa gaaacaacaa gatgtgcttg gtttccatga agccaacaaa 300
ataggatttg aagaaaaaga tattgcagcg aatgaagaga atcggaagtg gatgagagaa 360
aatgtacctg aaaatagtgc accagccaca ggttaccctc tgcccacctc gattttcaat 420
gaagccagt atcgcgggga ctatgatgcc ttctttgaag ccagagaaaa taatgcagt 480
tatgcttct taggcttgac agccccacct ggttcaaaag aagcagaagt gcaagcaaa 540
cagcaagcat gaaccttaag cactgtgctt taagcatcct gaaaaatgag tctccattgc 600
ttttataaaa tagcagaatt agctttgctt caaaaagaaat aggcctaatg ttgaaaaaat 660
agattagtgt ggttttcaca tgcaaacatt caaaatgaat acaaaattaa aatttgaa 720
ttatggtgat tatggtgag agaatggggt attaacataa aattatatta ataagtaga 780
atcgtagaaa tagtgttgtt acctgcgaag ccactcgtga tacaccaatg attttcaaaa 840
gaaaacaccc ttccctcctt ctgcccattac tatggcaact taagtgtatc tgcagctcta 900
cattaaaaag gagaagagaa aataacctgt ctctcattcc taagtgtcct cattatatt 960
catgaacaag aatatgtacc tttttgatgc tatattactg cgattaaaaa gttccttgca 1020
gtaattgttta tgatatgtta aacgttgtaa tttctatcog taattataac attcccatatt 1080
ttttgtagat gaaccttcta catattgaac cacagatttt ctgagctctc aaatgtagcc 1140
tttcattgca catttcagtg atcagaatag atatcctttt acacgcacaa aagcaataga 1200
ttcattcagt ggacaagttc cttgtttaac tacacagctg tgatggaaat atatatccaa 1260
gttccctggc tcaagtgaat atgcataatg atatcatgaa agtgggatgc caagtaagct 1320
taaaatggca ttctctagca aagagattag actttttaa aactgttata aaacagggtg 1380
ggcatcattt cccaagattg gtttcccttg agtttttgct aaaaacaaatc ttagtagatt 1440
tgcccgttta aaacaactca caatcgtaaa tgctactatt cctaagatat cttacctttt 1500
tatttcagtt tagccatgta ttgtatgagt gtattagtct aagcagtgag aatcttttct 1560
atgcctctat tccagcaaaa agtagaagta tcaaatataaa agggccaact ttaaaatatt 1620
aagccctgaag acctctaaaa agacaagaaa catggccctaa ataaaccaac tagatttaca 1680
tagtaagttt cacactacct tattaccaaa agcaaacacc tcttacttta aactacatta 1740
tcatgtatat ctattgtatg ctggtcttta ctttttgcca aaatcaacat ataatgaaga 1800
gatgcctttg tttcatgaga ttcaaacctg atgctatgct ttaaaataaa ctcagtactt 1860
ttagaaacat aaaaaaaaaa aaaaaaagcg gacccccoga gtatgtgggc cgcgcocggg 1920
gatttttccg gg

```

## (2) INFORMATION ON SEQ ID NO. 126:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 3024 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```

atatatgtta agacattccc ttgctaatta ttttctcttc tgttgttcta tttttttggt 60
ccagtttgct gtttttaaaag ttttgagtc cagctgggtcc tgtacattta actgaaaaaa 120
aagttaactta aaataatata aaaatagcac tcatgtatgt cctacagtta taggtgaaat 180
ttgatacttgt ttgtctttaca tagcatacct atagacagct taagttaaagt gactgttaaag 240
aggggttatgc ttatttgatga actctgttag ttgtttacca gctctgttag tatagttaa 300
ttgatctcag tagcttcaag tatttataaa atggttgaag tccaaatata tgtgataatt 360
acaaacacact ttgaattaat ggggggtggg aggctagttg aaatgcattt tatttaccoc 420
aggagtatgt taaaatgata gttataaatg ttggaagttt aaagcaagat actcagttta 480
gttcttttaca aatcataaga agaacaaaaa tagatgttga cattgtctatt tttaggtgtg 540
tggtttccat atgcttcttg ctttccctgt cacaggtggt gccagcaata ttggtgtgat 600
tgagggttat tggcaccac tgcacacacag gcgcacaatg gtgttagctg gccagaaaga 660
tggtgcatctc tggctaccgg gctgggggag acctttacca taggtagaag taacctgtgca 720
ttcggctgca aggtgtactg tacgtacaca ggtgctggct gatgtccact ttctgctttt 780
ctttctttct tttttctttt ttaaaagtaa tttcccccac agtaaaatcac actgactcct 840
gagtaaatgt attttccagt ttatggaaat tgggaatctg acaagtgaaa ccaatttaat 900
gtaaagtatt tggcttcaa atggtttctc tgtgctatgt ttgggaattc ttccagattc 960
cagagatatt ttacgtcttt gattcaattt aaaaatttga cttattttct tttagaaatal 1020
atgtattgtg tctgtgcaga aaaaaaaaaa ccaaaaaggga ttgctttact ccaagaggag 1080
agattgtctt aggataaaac tccaaagctca catttaatat aacagactga agtaaacatt 1140
agaaatctgt tttagactat tctgcacagt taactactga tctttagaat ctaaaaattg 1200
atatgaacct attcttaaat aattgaaccg ttttatattc aaatgactta tgatcggtgt 1260
tagtttggga aaaaataagat ggttaaattt tgatttaatt aaagttaatt gtattttttt 1320
cataaaatag cattttcaat ttgtaatgtg gtttaacatc cttgtgtgtt gccaaagaaa 1380
ttctatttgg ctgtgaatat tctatttgct tgcagtatct gtctctcttc cttaggctca 1440
gttggtgacc caagcctatt gtaaaccaat gattatctca aaggagatg ccaatggagt 1500
aacaaattgt taaccttcag tttctgtctg gtatatcttt ttaaaaaatc ggtagtttct 1560
ggaaaaaaaa gagaaggggg tttgtagtac ttaaccttat ttatttccgt atattttagt 1620
taattagttt ttggaataaa tggatttcag tatagctttg tggttaaatt gcattgacct 1680
tattttatgt ttaggcttat ttttaaatca acattttaaca gaacactttg aactagaatt 1740
tgcattgtct ccttaataaa cttaaagact gattttaatc tgactatgac actgagcata 1800
ttctttaaat tactcataat ttaataatgt taataatac taatttaaat tttagcagttt 1860
tagtataaga tgtgaccttt tgtctctgtg atgtctgaat gaagctataa cacttgacct 1920
tttatgcag gttttccctt ggaatatgga taaatacacc atgatacga aactgaagg 1980
acatcaccat gatgtggtag cttgtgactt ttctcctgat ggagcattac tggctactgc 2040
atcttatgat actcagatat atatctggga tccacataat ggagacattc tgaatgaatt 2100

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tgggcacctg tttccccac ctactccaat atttgctgga ggagcaaatg accggtgggt2160
acgatctgta ccttttagcc atgatggact gcattgtgca agccttgctg atgataaaat2220
ggtagaggtc tggagaattg atgaggatta tccagtgcaa ggtgcacott tgagcaaatg2280
ctctttgctg gccttctcta ctgtagggcag tgttttagct gctggggcac atgacggaag2340
tgtgtatttt tggggcaact caccgcaagt ccttagcctg caacatttat gtgcctatgc2400
aatccgaaga gtgatgccca cccaagaagt tcaggagctg ccgatttcct ccaagctttt2460
ggagtttctc tcgtatcgta tttagaagat tctgccttcc ctagttagtg ggaactgcag2520
aatacactta acacaaacct caagctttac tgacttcaat tatctgtttt taaagacgta2580
gaagatttat ttaatttgat atgttctgtg actgcatttt gatcagttga gcttttaaa2640
tattatttat agacaataga agtatttctg aacatatcaa atataaaatt ttttaaagat2700
ctaaactgga aaacatacat accctgtacat atttagatat aagctgctat atgttgaatg2760
gacccttttg cttttctgat ttttagttct gacatgtata tattgttcca gttagagccac2820
aatatgtatc tttgctgtaa agtgcaagga aattttaaat tctgggacac tgagtttagat2880
ggtaaaatct gacttacgaa agttgaattg ggtgaggcgg gcaaatcacc tgaggtcagc2940
agtttgagac tagcctggca aacatgatga aacctgtct ctactaaaaa taaaaaa3000
aaaaaaaaa aactcgaaac tact 3024

```

## (2) INFORMATION ON SEQ ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 505 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ctgcacgggc gcagatgtag gcaccggctc gactgcctgc cctctgtccc cggggctggg 60
tctctgtctc tccggttcct gggctcctaa tctctgttcc agcttcttcc aggtctgcgc120
gtctgttgtt cccagcgctc tgcgaagctg aaaaaggaga gcaacctgtc cagaatcccc180
gcaggacagg aaaaaggagg gaaatctcga catggaaaaa ctctacagtg aaatgaagg240
aatgcttcca aaccaggaaa agatggaaaa tgaagaacag ccacaagcag agagaaagcc300
agaagtaact tgtactctgg aagacaagaa gttgaaaaac gagggaaga cagaaaacaa360
gggcaaaaaa ggagatgagg aaatgttaaa ggataaagga aagccagaga gtgagggaga420
ggcaaaaaga ggaagtcag agagggaggg agagtcagag atggaggagg tcgagagaga480
gggaacccga ggtaggggaa gcgga 505

```

## (2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 115 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

PPLRLRLEFFY LRFISTSTA EIRKWRFGQ IILYEMDPHT TSFLIQARYN IIPGFSKSSQ 60  
 HGYLECYSVLA FIAASSERRA FFSKFKLVKV SCLWAAFLPS ITMKMHPTTV RAIIR 115

## (2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

VRDGAPGLSC GFVQNPFILF KSELLVSLAD EETSLSHNLK QLPAARRRPL RLPMATCYSA60  
 DQRRTPGTV ALVSSMSPSV GV 82

## (2) INFORMATION ON SEQ ID NO. 131:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 53 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

GIITLSLLMI IHPQMEEFIR QPLQFRLKTG AHRTQGTIKE DQEPFFLSK NWP

53

(2) INFORMATION ON SEQ ID NO. 132:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

LFILRWRSLS VSHFSFVLKQ EPTGPKELLR RTRNLGFFFQ KIGPSPINEG KN

52

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

KKKPRFLVLL NSSLGPGVSC FKTKLKLWTD KLLHLRMNNH Q

41

## (2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

ADPAFSTDLF QGCTDMAAAF RKAAKSRQRE HRERSSDYRK KQEYLKALRK KALEKNPDEF 60  
 YYKMTTRVKLQ GGVHIKETK EEVTPEQLKL MRTSGRQIYR KGRGCRS 107

## (2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

RIRRSPLIFS KAVQTWRLRF GRRLSPGSGN TESEAVTTVK NKNTSKLEGR RLLKKIQMNS60  
 TTK 63

## (2) INFORMATION ON SEQ ID NO. 136:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

LFWGYFFLSL LNNMYSTLEF NPSHFVVEFI WIFFKSLLEPK SFEVFLFFTV VTASLSVFPL60  
 PGLSRLPKSR RHVCTALEXI SGERRIR

87

(2) INFORMATION ON SEQ ID NO. 137:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

EANNYMSCQG GSRFHSFSIL PQYPGINAAT GGQSLFVLLP TPLFLCLFNS VKLFCLGPCK60  
 EPKENLSGQV HEWNAENILK ARFLEYSQLA FFPLI

95

(2) INFORMATION ON SEQ ID NO. 138:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

NSSASSPQFW PNSRLAVFTW YPGVGLLTLLI SMMFSKMKLD KVDHQLHRVF CKSIVSKWPR60  
 DLRKIQIFCL PWSCFKS

77

## (2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 133 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

DLKQDQGGKQK ICIFLKS LGH LLTILLQKTR CSWNSTLSSF ILENITIEIKV SNPTPGYQVK 60  
 TASLLLGQNC GLLAELFYGL QSKWSYLTHK MTKVLNLVRG KVLNIQFWIQ EIIIVNFPFK120  
 SMERMLVENI LK1 133

## (2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 783 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

FLLPQSAFHL YEPPLDYMT WRMGPRTML LAMWLVCSE PHPHATIRGS HGGRKVPVLS 60  
 POSSRPARFL RHTGRSRGIE RSTLEEPNLQ PLQRRRSVPV LRLARPTEPP ARSDINGAAV120  
 RPEQRPAARG SPREMIRDEG SSARSMLRF PSGSSSPNLL ASFAGKNRVW VISAPHASEG180  
 YYRLMMLLKK DDVYCELAER HIQIVLFHQ AGEEGGKVRR ITSEGQILEQ PLDPSLIPKL240  
 MSFLKLEKKG FGMVLLKKT L QVEERYVPV RLEAMYVID QGPIRRRIEKI RQKGEVQCKK300  
 ASGVEGQVVA EGNDDGGGAG RPSLGSEKKK EDPRRAQVPP TRESRVKVL R KLAATAPALP360  
 QPPTSPRATT LPPAPATTVT RSTRAVTV A ARPMTTTAFT TTQRPWTSPS SHRPPTTTVE420  
 ITARRPSVSE NLYPPSRKQD HRERPQTTRR PSKATSLSEF TNAPPTTISE PSTRAAGPGR480  
 FRDNRMDRRE HGHRDPNVVP GPPKPAKEKP PKKKAQDKIL SNEYEERYDL SRPTASQLED540  
 ELQVGNVPLK KAKESKKHEK LEKPEKEKKK KMKENADKL LKSEKQMKKS EKKSKEKEK600  
 SKKKKGKTE QDGYQKPTNK HFTQSPKKS ADLLGSFEGK RRLLLITAPK AENNMYVQQR660  
 DEYLESFCMK ATRKISVITI FGPVNNSTMK IDHFQDNEK PMRVVDDIDL VDQRLISELR720  
 KEYGMTYNDP FMVLTDVDLR VKQYVEVPIT MKSVFDLIDT FQSRIKDMEN QKRGVFEGG780  
 KTP 783

## (2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

KMVVGVMVFL RWERMENLF QGNGFAAEVR MCSCIDLQTP RRWVHTACLG VPRDSRPPTY60  
 LSEARAAGHG PSAKPVCDAL GALVQEA 87

## (2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

SFSSGLVRNT LFITTFKFLY FFSSMLVLMT FGDVSVRAGE RGVRRPSHRW SWPPPALSLL60  
 PDHRFPICPS ENLSQGELKF TGQGTSTFIYF IMLANRT 97

## (2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

ASCTKAPRAS HTGLAEGPWP AARASDKYVG GLESLGTPKH AVCTHLLGVC RSIQEHILTS60  
AANPFPWKRF SHILSHLKKT HTPTTIF 87

(2) INFORMATION ON SEQ ID NO. 147:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 119 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

NSKDKCFSLA FITTPETERW RCCASEPRL ALKHQGHRTQ AWQRGHGQRH ELQTSMLEVS 60  
NPLAPPSMQC APTFWVSADR YRNTSLPLQR THFPGKDFHT SSPTSKKPTH PQPFFKAPR 119

(2) INFORMATION ON SEQ ID NO. 148:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 87 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

STKGIAHRLG RGAMASGTSF RQVCWRSRIP WHPQACSVHP PSGCLQIDTG THPYLCSEPI60  
SLEKIFTHPL PPQKNPHTN HFLKPHG 87

## (2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

DPPSHSQLGR CCHRMVFESV GARAHFWLSQ QLGWHLPLSA RNSNIMNARD SVLSKVFHFK60  
GAGHGCSRL 69

## (2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

SAHLGLPKCW DYRREHPCPA PFGWKTLLST LSLAFIMLLF LALGSKCHPS CCDNQKCALA60  
PTLSNTIR 68

## (2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

HHTQPIFVFL VATGFHHVQG AGLEPLTSGD PPTLASQSAG ITGVSTRALP LLDGRLY 57

(2) INFORMATION ON SEQ ID NO. 152:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

SAGIPKLAPK IPLPFSOLLK CYLISGAFFD HTLKTSTPTH GPCPPSRLHF LAYTYQM 57

(2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 32 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

LKTLTVASI RVSTFYSSDP TSFNLLLIY GG



## (2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 32 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

TKRAVMKSMH LCAIRAFLLVP HSELIDSDYI HF

32

## (2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

GRVRAVKGRH SDRSHSQQCF QSVNTDEVPT T

31

## (2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

VQNVMSACNF IFIKAKLIYM EYCSIYYAPI YILSPVVRYF ISLLLNIFYT YL

52

(2) INFORMATION ON SEQ ID NO. 157:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 59 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGTECFFICC IENSHTQFSI LQCSHHGWT LGRNSPQPFL VSFSQFFSVS RWAPVINLP 59

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 38 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

LSLCPWPNGN FFQWCLLEEV FSSGQFKEIK LGNGEGGR

38

## (2) INFORMATION ON SEQ ID NO. 159:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

GSILMMQEI SSWSQKFPRG AVFLRNGVYL NNS

33

## (2) INFORMATION ON SEQ ID NO. 160:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

KKLPQGQGHK LNYLNLKLF LKIQHLLGTF DSRKRFPASY PKCF

44

## (2) INFORMATION ON SEQ ID NO. 161:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 225 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

AAGGLGLGVG PRGMWRAGSM SAEGLVGCAL RAVNERVQQA VARRPRDLPA IQPRLVAVSK 60  
TKPADMVIEA YGHGQRTFGE NYVQELLEKA SNPKILSLCP EIKWHFIGHL QKQNVNKLMA120  
VPNLFMLETV DSVKLADKVN SSWQRKGSPE RLKVMVQINT SGEESKHGLP PSETIAIVEH180  
INAKCPNLEF VGLMTIGSFG HDLSQGPNDP FQLLLSLPEE TVVKS 225

(2) INFORMATION ON SEQ ID NO. 162:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 99 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CRGPGARRRS PGDVESWQHV GRAGSRVRIA GGERARAAGC GAAAAGSPSH PAPASGGQQN60  
QTCRHGDRGL WTWAAHFWRE LASGTARKSI KSQNSVFVS 99

(2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 120 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

LRSCPGLPMV ISPTNSRLGH LAFMCSTMAM VSEGGRPCLL SSPLVLIWTI TFNLSGEFFL 60  
CQELFTLSAN FTSTVSSMK RLGTAINLLT FCFRWPMMC HLISGHKDRI LGFDAFSSSS120

## (2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 75 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

TSTGPFSSPLV ASAATELAAF AAFSSACMR PEGSASLFWN RLPLLMFGDL QGCEAREGIA60  
MRILQASFSG LSSKG 75

## (2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 90 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

NTHGDALTCL TPLQVPKHEE GKAIPKQRGR TFRAHTCRAK GSGKSCQFSC SRGYQGAGGT60  
SAGLALYLHT RTAASRGTSF SPVGSVAPQQ 90

## (2) INFORMATION ON SEQ ID NO. 166:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

SHPFEDSPEK EACKIRMAMP SRASHPCRSF NMRRGRRFQN REAEPGRIH AELKAAAKAA60  
SSVAAEATRG LEGPVLV

77

## (2) INFORMATION ON SEQ ID NO. 167:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 347 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

TAFPLFVVVA AVLWGAAPTR GLIRATSDHN ASMDFADLPA LFGATLSQEG LQGFLVEAHP 60  
DNACSPIAPP PPAPVNGSVF IALLRRFDCN FDLKVLNAQK AGYGAAVVHN VNSNELLNMV120

WNSEEIIQQI WIPSVFIGER SSEYLRLAEV YEKGARVLLV PONTFPLGYY LIPFTGIVGL180  
LVLAMGAVMI ARCIQHRKRL QRNALTKEQL KQIPTHDYQK GDQYDVCAIC LDEYEDGDKL240  
RVLPDAHAYH SRCVDPWLQ TRKTCPIQK PVHRGPGDED QEEETQGQEE GDEGEPRDHP300  
ASERTPLLGS SPTLPTSEFS LAPAPLVFFG PSTDPPLSFP SSPVLV 347

## (2) INFORMATION ON SEQ ID NO. 168:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 588 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

QVTNMSDKSE LKAELEKQKQ RLAQIREKK RKEEERKKKE TDQKKEAVAP VQEESELEKK 60  
 RREAEEALLQS MGLTPESPIV PPPMSSESSKS VSTPSEAGSQ DSGDGAVGSR RGPiKLGMAK120  
 ITQVDFPPRE IVTYTKETQT PVMAQPKED EEDDDVVAPK PPIEPSEET LKKEENDSK180  
 APPHELTEEE KQQILASEEF LSFFDHSTRI VERALSEQIN IFFDYSGRDL EDKEGEIQAG240  
 AKLSLNRQFF DERWSKHRVV SCLDWSSQYP ELLVASYNIN EDAPHEPDGV ALVWNMKYKK300  
 TTPEYVFHCQ SAVMSATFAK FHPNLVVGTT YSGQIVLWDN RSNKRTPVQR TPLSAAATH360  
 PVYCVNVVGT QNAHNLISS TDGKICSWSL DMLSHPDQSM ELVHKQSKAV AVTSMSEFPV420  
 DVNNFVVGSE EGSVYTACRH GSKAGISEMF EGHQGPITGI HCHAAVGAVD FSHLFVTSSF480  
 DWTVKLWTTK NNKPLYSFED NADYVYDVMM SPTHPALFAC VDGMRGLDLW NLNNDTEVPT540  
 ASISVEGNFA LNRVRWTHSG RGGGCGGILK DKFCYFAMLG GAVCWSPQ 588

## (2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 41 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

FHVEQLSHSF LSWRKDTIQR GSKDFVKRGI HNLLWSKCPH L

41

## (2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 55 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

CPRDVGTCISI VNYGCHVLQN PYCPFELCPs SKIRSYDSIV QHGIMKSLs SSIFP

55

## (2) INFORMATION ON SEQ ID NO. 171:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

KAFLVLSFPK WALFLVIHMT LFGCGCLLNF LEWTSFSKPK PARDRKGNGN

50

## (2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CTFNIESFIY LIVYRTFPHY THLLNHLTS IFKFFCTSSF SFNLVKPVIH TNVYCELSG60

## (2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes



- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

EESFVFLIHS FVNRYKGTNV LTYTKKKKIL VYPLMLIHRV LSYNVIQLGS LTFFPKNIFI60  
EKGITLS 67

- (2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 56 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

LYHIIRKHSV DQHKWVHKNF FELGVCKHIC SFISVYKTVN QKDKTFFLVF VIFFLN 56

- (2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 289 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SRRTQGAAS RFPQFDITGQ DFSASAQRGG LVAHSOLDER AIEALKEFNE DGALAVLQQF 60  
KDSDLSHWQN KSAFLCGVMK TYRQREKQGT KVADSSKSGPD EAKIKALLER TGYTLDVTTG120  
QRKYGGPPPD SVYSGQQPSV GTEIFVGKIP RDLFEDELVP LFEKAGPIWD LRLMMDPLTG180  
LNRGYAFVTF CTKEAAQEA V KLYNNHEIRS GKHIGVCISV ANNRLEFVGS I PKSKTKEQIL240  
EEFSKVTEGL TDVILYHQPD DKKNRGFCF LEYEDHKATA QARRRLIEW 289

## (2) INFORMATION ON SEQ ID NO. 182:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 39 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

KLCTEWLKVIGIWRWVRGSC LGRLOFTWIR VGLREEIGV

39

## (2) INFORMATION ON SEQ ID NO. 183:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 42 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

EAVMTLILIL HTYFLTQPYSP NPSEAKPSQT APSPSPYPF NL

42

## (2) INFORMATION ON SEQ ID NO. 184:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

PSFSFYTPIS SRNPTLIQVK QSLPRQLPLI HLHIPPTFNH SVHNFYSLHT SYLLIFLTNKG60

(2) INFORMATION ON SEQ ID NO. 188:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 46 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

RSRFHMMTL RALQLSLPTK IGGACFRVSR LSPTEKKKKK MSLEEA

46

(2) INFORMATION ON SEQ ID NO. 189:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 65 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ITFSHDAHAQ GASIIPPHKD RWRVFQGLSS LSYRKEKEKN VIRRGVTRQS VPRFVFPGVA60  
ERDQF

65

## (2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 66 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ECREAGPLFL QSRLELISFG HSRKHKPGDG LTCYASSNDI FFFFSVGER RETLKHAPPI60  
 FVGRDN 66

## (2) INFORMATION ON SEQ ID NO. 191:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

RQTEGETEML RKPSYTTLPR NTSLRECKKY YWRWKSARKTA MGRPRPGD

48

## (2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

RAETRSQGQL NEDKLGKLR CLESPAIQLY PEILPLGNVK STTGDGRAEK QLWAEQGQVI60

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

SCIAGLSKHL SFFFSLSLS CPWLRVSALQ LLPLRAFPFA SDLL

44

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 98 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EIMNGLVLDN IWFHKLLTSV LGESHFVNHT SEIYMLNGE QRRSCCKRCI KYLCCFCMRL60  
RSFSLSPFLF PIRISREAKL FCGFGNGHFP GKCIWIDD

98

## (2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 115 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

AHSSTKAKSK SEFLPILPLC NTLRSSHNCF TPHLPVSCCT KSPSLSSFYR IVRQGRRALR 60  
 RRAFEALSTL PASVKMRLHY SPEKRARFSH RSRCIFPGND HSQTHRTVWL LWISL 115

## (2) INFORMATION ON SEQ ID NO. 196:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

SGVKRISCVL ETKAYCHCFK KSLCEMKKNM TNTGSHTYTY IQRNLTCTH TGRYRHTVPP 60  
 KRSPNQSSYR FYHSVILSEV PTTAQLHTYP FPAAQSLLS HLFDTSSGRA EGHYAAEHSR120  
 LSAHCQPA 128

## (2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

RPGVEPPLLRLRPDSETQKR VQGWGEMWSE GRAFAFKGSS RTHWDIVTHL NHLLIERCWP60  
 PNNGRSGPGP RA 72

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 77 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

GPSFYARGPG PDLPLLGGQH LSIRRWFKCV TMSQCVLELP FSNANLPSLH ISPHFWTRFC60  
 VSESGNLLKR GGSTPGL 77

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 60 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

EANTFLSEDG SNVLQCPVSF SNFLSQMQTF PHSTSLPIPG FVSVSLSQAT FSKEGVPLPA60

## (2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 84 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

PTTTLVIPLF FLSSRRKRQK DSFQTALCSL HCSFPAQAAS TGKARVVTPY FSEVLLFHGV60  
 TLLSESKFRK QVLPLADKNH TSFL 84

## (2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 128 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CDRVPLFLSY WCAVADSWLT ASSVSHVKG I LSPQPTCAP PGPANCFNF FFFFFFFLVET 60  
 GSPSVAQDGL ELLGSSNPPT LASQSAEITG MSHYAQFEQD DLNLINSTPK QQLSLSQGCQ120  
 GGLCEGKD 128

## (2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

WVAGRRHLLS VQTKSLQVLG LDLCVTPESQ CIRLYYKLV WFLSAKGKTC FLNLLSDNKV60  
 TPWKRTSEK YGVTTWAFPV LAACFGKLQC RLQRAV 96

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

PDFRGFAGPA MFSRGFQVGR GERQGENAPC RGVQRSPASC PAVGWTSOL 49

(2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

QISGVLAPR CFPEVFKWEE ESDKVKMPRA GASSGVLPAV RRWGGRLIYE GAHPPI 56

## (2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

CCSCQSSQVR YSDRMMGTFI NQTSTPPPD S WQDSAGRP GT GHFHLVALL F PLENLWKTSR60  
 GPQNFGNL 68

## (2) INFORMATION ON SEQ ID NO. 209:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 164 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

WGGRTLASAV SIPLRKCHSH RPTVLARKQP QSGVPPPYTA IASPDASGIP VINCRVCQSL 60  
 INLDGKLLHQH VVKCTVCNEA TPIKNPPTGK KYVRCPCNCL LICKDTSRRI GCPRPNCRR1120  
 INLGPVMLIS EGTSSACIA QSQPEGYKGR VLHGHWGTHS LWDG 164

## (2) INFORMATION ON SEQ ID NO. 210:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 218 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

SSAVPDGAVG RPVAVAVGGP PHSCRCRPCC LMAAIGVHLG CTSACVAVYK DGRAGVVAND 60  
 AGDRVTPAVV AYSENNEIVG LAAKQSRIRN ISNTVMKVKG ILGRSSSDPQ AQKYIAESKC120  
 LVIEKNGKLR YEIDTGEETK FVNPEDVARL IFSKMKETAH SVLGSDANDV VITVPDFDFGE180  
 KQKNALGEAA RAAGFNVLRL IHEPSAALLA YGVGQDSP 218

(2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 186 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

RKWTLTSMQ KRMLKRPDNK LKYVTKWQRT AKQITHPFSR NSTMSSMNIT ILTSPSSSRK 60  
 YKRAEERRIV RMGESMKTYA EVDRQVIPII GKCLDGIVKA AESIDQKNDS QLVIEAYKSG120  
 FEPPGDIEFE DYTQPMKRTV SDNLSNSRG EGKPDCLKFGG KSKGKLWPF I KKNKLMSLLT180  
 GGPFSF 186

(2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ISGRRVSLNF VSEFSITEFC PCWCLGYRPD GPGSFSPSCSG LEVSPLHFLK ACVQCSPKSI60

(2) INFORMATION ON SEQ ID NO. 213:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 68 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

DLCSTLSATK GSITCFLNKA LVSPPASSGL HYSETNSTSF AGGITVPISR LGPALQTSFG60  
LLVLLTLL 68

(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 54 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TISFFKSKRG LKQEGTGTS QMDLGEHCTQ ALRKCKGLTS RPEQDGKLPF PSG

## (2) INFORMATION ON SEQ ID NO. 215:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 276 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```

LPTAFLLSSV FWIFMTWEL FFPDLAGAPF YFSFIFSIVA FLYFFYKTWA TDPGFTRKASE 60
EEKKVNIIIT AETGSLDERT FCTSLIRKE LRSLHCHVCN CCVARYDQHC LWTGRCIFGFI20
NHHYYIFFLF FLSMVCGWII YGSFIYLSH CATTFKEDGL WTYLNQIVAC SPWVLYILML180
ATFHFSWSTF LLLNQLQIA FLGLTSHERI SLQKQSKHMK QTLSLRKTEY NLGFMQNLD240
FFQCQCGFLV KPCVVDWTSQ YTMVFHPARE KVLRSV                               276
  
```

## (2) INFORMATION ON SEQ ID NO. 216:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```

SPSRSPVVFA GEFLFKHPFV EESLMSFFHP DLHLMNPKAI STQFLYSVF
  
```

49

## (2) INFORMATION ON SEQ ID NO. 217:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 37 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

KEINNYIRKE KNFKYLQFST PNHQDRWVQ KNAPEWF

37

(2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

KFSSKDDRTS RRRSIIISER KKILSIYNPL LLITPKIGGS RKMHLGFTEE RS

52

(2) INFORMATION ON SEQ ID NO. 219:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 150 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

DKRNGIISK LSPEKTLKS ILKRKGTSDI SDESDDIEIS SKSRVRKRAS SLRFKRIKET 60  
 KKELHNSPKT MNKTNQVYAA NEDHNSQFID DYSSSDSELS VSHFSFSKQS HRPRTIRDRT120  
 SFSSKLPSHN KKNSTFIPRK PMKCSNEESC

150

## (2) INFORMATION ON SEQ ID NO. 220:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

NKWNKSKLGK EISKATQSLD PAQLADPCHS LAVAASLCSL KGEFGQCFFS PWAWSLHSGK60  
 QTSGPFPEKSQ ECLAAWVLI AMF 83

## (2) INFORMATION ON SEQ ID NO. 221:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

NSKLVDCRM E TWLLRRHWVSF SLCVSCWGVV MIVSALTHCT RWQQDTALHK MAAPLQLFPQ60  
 PPSLHPHREFG LWFLSSVTYC LRS 83

## (2) INFORMATION ON SEQ ID NO. 222:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 90 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

CLHNREPDIF RILSSSYGI LRPRSYLQTK WPWSLQNIAM STHQARHSW DLGKGPLVCF60  
PLCSDQAQGL GKHWPGSPFS EHREATARE 90

(2) INFORMATION ON SEQ ID NO. 223:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 114 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

QSLRHCWLNI SLQRDGAFFE PGAGPVSSKA LDVFLVTRRR GCQMPLKPSG LVWPRAAGQG 60  
RAEKWSSSQL ALPSPTQPRP RWSLDSILTS ASPKVQMSKC LVVQSQEMGS YLKS 114

(2) INFORMATION ON SEQ ID NO. 224:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 145 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GCVGGGRAEA MAEKFHLEE HLEKFVENIR QLGIIVSDFQ PSSQAGLNQK LNFIVTGLQD 60  
IDKCRQQLHD ITVPLEVFEY IDQGRNPQLY TRECLERALA KNEQVKGKID TMKKFKSLLI120  
QELSKVFPED MAKYRSIRGE DHFPS 145



## (2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GQTMRTTEGLR GVSRAQSHLS RKVASALAVP ASRRIAVPGD LHTGRVSWLR RRVILPPDAS60  
ILSHVFRKYF RKFLNQAFK FLHGVDLAFN LLIFS 95

## (2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ALRPPLYALG QQVGAVTGPA DCSATAPLDF WIFWKQSQNS GLLGGWQRGM VRGPPFFISLF60  
SIRWQSTGHP WWVSGPRPMP TLPFESR 87

## (2) INFORMATION ON SEQ ID NO. 227:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

APALATQPPL SLPRGTGPAY LNSLTMLQT WLLDSKLLSS NVLLPHFHL HICLLLYWFL60  
LLNLYFHSWV LCLPFFFS A 79

(2) INFORMATION ON SEQ ID NO. 228:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 87 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

RSMSVEASFV CLGTTGRCCCH WSCRFSNSP FGFLDILETK SEQWPTGGLA EGYGKRTSFH60  
LPVQHPMAVH RSSLVGVPRK THAHLTL 87

(2) INFORMATION ON SEQ ID NO. 229:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 150 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ATLSRFFGRI FNLALTQVFP FLFSSPNDKK SFCISIEGEWN GVMYAKYATG ENTVEVDTKK 60  
LPIIKKKVRK LEDQNEYESR SLWKDVTENL KIRDIDAATE AKHRLEERQR AEARERKEKE120  
IQWETRLFHE DGEWCWYDEP LLKRLGAAKH 150

## (2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 206 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

DSLRRGLGIC LWEFIHLSLL FTSPKPGFPL LKPAVISQLE GGSELGGSSP LAAGTGLQGS 60  
 QTDIQTNDNL TKEMYEGKEN VSFELQRDFS QETDFSEASL LEKQQEVHSA GNKKKESNT120  
 IDGTVKDETS PVEECFFSQS SNSYQCHTIT GEQPSGCTGL GKSISFDTKL VKHEITNSEE180  
 RPFKCEELVE PFRCDQLIQ PSREQH 206

## (2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 57 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

RIRRSALIFS KGVQRWRRVF GRRVSPGSGN TESEASDYRK KQGTSKVFGR RVLKKIQ 57

## (2) INFORMATION ON SEQ ID NO. 238:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

GTLLFTVVTG FALCVPAAGT YPSENPPPS LYLTKDQCR TPDF

44

(2) INFORMATION ON SEQ ID NO. 239:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 74 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

NLYPTLEFNP SHEVVELTGF FSTPFFRTPL RYLVFYGSHW LRSLCSRCRD LPAFRKPAAI60  
SVHPWKRSVQ NAGS

74

(2) INFORMATION ON SEQ ID NO. 243:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 183 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

AAVAFGAKGT SPAEARSSRG IEEAGPRAHG RAGREPERRR SRQQRGGGLQ ARRSTLLKTC 60  
ARARATAPGA MKMVAPWTRF YNSCCLOCH VRTGILLGV WYLIINAVVL LILLSALADP120  
DQYNFSSSEL GGDFFEMDDA NMCIATAISL LMILICAMAT YGAYKQRAAG SSHSSVTRSL180  
TLF

183

## (2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 157 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

QQHVVHCHCDF SSHDPDMCYG YLRVQVQATRS WIIPFFCYQI FDFALNMLVA ITVLIYPNSI 60  
 QEYIRQLPPN FPYRDDVMSV NPTCLVLIIL LFISIILTFK GYLISCVVNC YRYINGRNSI120  
 DVLVYVTSND TTVLLPPYDD ATVNGAAKEP PPPYVSA 157

## (2) INFORMATION ON SEQ ID NO. 251:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

ATKTVPRQRW SPPHCPRPNP SLNLLRCGWG NRGKTEAPDA FSLLCSSAID CPDVQRETHT60  
 RFAHENWGAD GQADRLCLFS E 81

## (2) INFORMATION ON SEQ ID NO. 252:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GVDGETEAKL RHLMSACCA AVPLTALMFR EKRTQGLPMR IGEQMAKQIG YVCFLSDEVR60  
KPCGSGGHLW FILFFYPWLL EMVTFRVQL HlseHYC 97

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 114 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

LEILGIFSRV SKLSSSPDT HPSSQIGVAI LGGRVVYGTG GCLHISQNYF RTIVPKSRVF 60  
TGRQNLFSP VPQLLSQIPI LGSHQLPIPH QTATVPSLSP YCSFKSCSQE RNCH 114

(2) INFORMATION ON SEQ ID NO. 254:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 53 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

IPSPQGPFCR SYSDPRKCPF PIVVLCLWGL VYPRGNCGEI IGLRVKRALV LEL

## (2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 35 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

QVDTIISTRK GLKLQNQC SL DSQTNDFTV TPGID

35

## (2) INFORMATION ON SEQ ID NO. 256:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 41 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TKPQRHRTTM GKGHFLGSEY DLQNGPCGLG IYPYAVFWSN A

41

## (2) INFORMATION ON SEQ ID NO. 260:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 205 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

GSVKVPASPR PGGTSLGPFV AAKELSFSPR NGRGQLPRP PGSLLTLLFF SSPASRGPAS 60  
LSPGGIRLLL PPPPHLLPGQ PACPAAVMCD KEFMWALKNG DLDEVKDYVA KGEDVNRTLE120  
GGRKPLHYAA DCGQLEILEF LLLKGADINA PDKHHTPLL SAVYEGHVSC VKLLLSKGAD180  
KTVKGPDLGT AFEATDNQAI KALLQ 205

(2) INFORMATION ON SEQ ID NO. 264:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 180 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

RNMSSFSRAP QQWATFARIW YLLDGKMQPF GKLAAMASIR LQGLHKPVYH ALSDCGDHVV 60  
IMNTRHIAFS GNKWEQKVYS SHTGYGGFR QVTAAQLHLR DFVAIVKLAI YGMLPKNLHRI20  
RTMMERLHLF PDEYIPEDIL KNLVEELPQP RKIPKRLDEY TQEEIDAFPR LWTPPEDYRL180

(2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 78 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

VIGYPSRINS EPSPIYINRP GNNVKLNCMA MGISKADITW ELTDKSHLKA GVQARLYGNR60  
FLQPQGSMTM SACHKEGW 78



## (2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 40 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

ATPLCGMLNG SLIPGVEEIC FHTDEPEPLP SDATYPLTPT

40

## (2) INFORMATION ON SEQ ID NO. 267:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 136 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

VGIWQEDHLP QSLGFLNKKE IVFLSWLLRL LKLALPLKYD ISFAVLNLKL VASSVAHFQF 60  
 LYQASLLSFP LRMGQVCSGG HSVRFSRGFG RGFKGKYS GG RMGSGVKVGD KGGRAKGGVE120  
 GWGPYLD RGM FGGQ GK

176

## (2) INFORMATION ON SEQ ID NO. 268:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

LVYFKQGTKE PGKRSGHVKR DTQDTLRDQS GSTPVLLPEC LCVNFCFLQN KRQQRKLLNQ60  
 NTDPMRNGAC FCDPGLSAR LQELTDGQLL IF 92

(2) INFORMATION ON SEQ ID NO. 269:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

NLVYTMWLQI YVNVHFEHIY VLNKEMLVTK IRFTLKEEF YSKHSNLFK CFKIQSIVFK 60  
 VAVKASTYVK TQKEGSSDRN TAPLLCCFSC SLYTLKHLL SGA 103

(2) INFORMATION ON SEQ ID NO. 270:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

FIYQSKVRD IFAVTLAILS LQSPTSRVQC TSNNSLKTRH LTISVYLCK VNKSSIIKE60  
 LCFYQRLSPS EFLHKLMPSL QL 82

## (2) INFORMATION ON SEQ ID NO. 274:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

QQHHLPSQSLG FLNKKKEVVFL TWLLRLLLKLA LPLKYDISFA VLNLKLVASS VEHFQFLYQA60  
 SLLSFPIRMD MCCSACHVCN ASCREFGHSI KEKIQ 95

## (2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

LLRQYHTSSF YTKPVSSVFP LEWTCVQRV MSVMLHAESL VIVLKRKYSE VTMSPE 56

## (2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

HAEQHMSILM GKLRRLAWYR NWKCGTDEAT NFKFRTAKLM SYFKGRANFN NLNNQVKNTT60  
SFLLRNPND 69

(2) INFORMATION ON SEQ ID NO. 277:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

YILEISPLKP SLAPTSGLM PQGFPPHECN PRYPSLSTPS QTPTPGIARE DFGLANCVGY60  
VSVVLIRDVH DCQSAFLTSV TTLRCNSSQ KKTFS 95

(2) INFORMATION ON SEQ ID NO. 278:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 133 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

PTQFARPKSS RAIPGVGVWD GVDNEGVLGL QKWGGNFWGI SPQEVGASDG FRGDISNIYQ 60  
PWALSPCCSQ HGPHTSSLRL TWELVRNAGS PRSIELEAVL TRSPVIFMAQ SSFLRDRCLL120  
LSAGMRHPWG RCG 133

## (2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 102 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

LKQHSNQHNN LLGQSLHGQS LGWESGMGWI MKDTWGCRCRG VGIPGASVHR RWGPAMASGV 60  
 IFPIYISPGH SRPAAHSMVL TPAASALPGS LLEMQDLPLD LS 102

## (2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

VYSANEGQNF QFIDGYSAAD ESLCVSHFNF CKQRHRPRTV RGRTSFSSKL PRHNKENSTF60  
 ISRKPMECNSN EEVNVQGSQD GSMGKF 86

## (2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 69 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

GAEIVFLQNC LGIIRKIALI FQGNRWNVQM RKLLIKSRM DQWVNFWRQ GGAYIHSNPD60  
VIWSGGQWK 69

(2) INFORMATION ON SEQ ID NO. 285:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 59 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

LTSSFEHSI GFLEIKVLFS LLCLGNFEK LVLPLTVLGL CLCLQKLKWL THKLSSAAE 59

(2) INFORMATION ON SEQ ID NO. 286:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 65 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

GKEPQPESNS IMVKFPTSS CEWVIRKNE PDKNQRQMG SVTGSLSL NPIEYCGLT60  
CQGGD 65

## (2) INFORMATION ON SEQ ID NO. 287:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

FLSFGSSFFL ITHSQDQSVG NLTMIELLSG WGSFPHRKDI LKTKKYLN

48

## (2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 32 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

ARNIQSDLEW MIKIQSQTPS VFDFCLLDPH FS

32

## (2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

CAKLETGDFD LSYLFAFCAS PSNLVHLSSH SCYFQVKQDI LGVKSLWVFC FYVYKNGFCV60  
 PEPCKYQLIW KLTIIM 76

(2) INFORMATION ON SEQ ID NO. 293:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

VELSLLFPQL SQLLVNFKEA GHDDSHLLSQ NFGRRRWADS LSPGVQDEPG QYGPTSSLTK60  
 HPH 63

(2) INFORMATION ON SEQ ID NO. 294:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 73 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

PPKCLVSLN NMNETKDEPD YLVTHRRRTS SSGNQILFQA WHIKGKKGSE RRVRYHLKPF60  
 QKIWQKTASK SIR 73



## (2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 132 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

PLGPASSAFG FSGSKSRSEE GRDGTASPGT FKYHPWSPLS SLREWTSQST SSGLSDLLLC 60  
 LYQPWQGSRI HLVGSGPSQY HWGSNKFLEP QSLGPGSQLI GDGVVFQARA EFGTSGHELE120  
 GNSVSYELGP WP 132

## (2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 70 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

ESRRGALAGP LSKAGEGRPG WYLNVPGLMS HPFLPHSYSL TLMAKARDAG PKGKNVLSVF60  
 SGFYSLVSLH 70

## (2) INFORMATION ON SEQ ID NO. 300:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 143 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

GVKAREYRED VFTFRACVSG FGHQQRVGV RKEGMGQHPW DVQVPSWSFF SSLREWTSQS 60  
 TSSGLSDLLL CLYQFWQSSR IHLVSGGFSQ YHWGSNKFLF PQSLGPGSQL IADGVPFKLVI20  
 PARAEFGTSL KGNSTVYELG PWP 143

(2) INFORMATION ON SEQ ID NO. 304:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 408 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

FANWEFMGTE QLQPQLPSFK VWSRCRCRQG PTKFNQVSRM QTPAPVSRRV GLAVSLTPPP 60  
 SGQSGPSVMG KAAACPATPA SAPSQGLSFG GPVSCWPGSP LLHLIGGRQL LDLCPCGGRS120  
 LPFSSSSSSS VNSDSAPDGP RGLGCFGGVV LGGRGFKYLL YFLFVAATQQ ILLGRASAF180  
 LKRDVGDPDV VAPAFFAVAG HLHQAVALPG VRVRVRDQET MQVSGLGGAL GLGRLSQELR240  
 QALHARHPHD VDVVVTAEGE DEREVDLQGD VILLLLVNGQ EAEDHAVVWH IHQLGRLVHP300  
 HCEAILALSG HQKLLHRGGH RLHLRRVVA RHELFQRHVA IIIHSGCGST AVPREKLQNP360  
 SQRAQNLPTF LERSKTEFGK QRNFSRKGGK IYCKVLGEDN PGSCGNQR 408

(2) INFORMATION ON SEQ ID NO. 305:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 169 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

GWGVWQAGLD PVLGPPSSAV PSLLLGVVSM VWPHLQLCLS AVPLASSSLN SAANSPVSSR 60  
 ARQGWWGWCW QQLLSWCDLS GLHLRGRNGP GYRGQIHFGW SPRPPGLGAA GGRWLLVGRW120  
 PSCLACLPCL SSSPNALSVS AFLAPGLSTP SAYKAVSPFQ TTVWLQPIR 169

(2) INFORMATION ON SEQ ID NO. 306:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 120 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

ILQLGHQFPL VPARAGAVGV GSSFSLGATF PASTSEVGMG QAIEVRFIQA GVLVLRAWGL 60  
 LGGAGCWWEG GHRAWLVFPA SLLLLTLCLS LLSWPRASPL PQLIRLCLLL RPQSGSSPSG120

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 472 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

SESLTHPGEE PGGFFPGGAP TMATPLVAGP AALRFAAAAA WQVVRGRGVE HFPVRLEFLR 60  
 SLRAVAPGLV RYRHHERLCM GLKAKVVVEL ILQGRPWAQV LKALNHHFPE SGPIVRDPKA120  
 TKQDLRKILE AQETFFYQQVK QLSEAPVDLA SKLQELEQEV GEFFLAAMEK LLFEYLCQLE180  
 KALPTPQAQQ LQDVLSWMQF GVSITSSLAW RQYGVDMGWL LPECSVTDSV NLAEPMEQNF240  
 PQQRLALHN PLPKAKPGTH LPQGFSRTH FEFLAGRHFN LAPLGRRRVQ SQWASTRGGH300  
 KERPTVLMFF FRNLGSPTQV ISKPESKEEH AIYTADLAMG TRAASTGKSK SPCQTLGGR360  
 LKENFVDLPA TEQENCLDC YMDPLRLSL PPRARKFVCP PSLCSSLVIT GDVLVDSDEE420  
 ENGQGEKES LENYQTKTFD TLIPTLCEYL PPSGHGAIPV SSCDCRSDSSR PL 472

## (2) INFORMATION ON SEQ ID NO. 308:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 138 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

PGFALRGAIG PREGRGGGRG YRRSSGRQPL VSWQRQARCG SGGAMSFCSF FGGEVFQNH 60  
 EPGVYVCAKC GYELFSSRSK YAHSSPWPAF TETIHADSV KPEHNRSEA LKVSCKGCN120  
 GLGHEFLNDG PKFGQSRF 138

## (2) INFORMATION ON SEQ ID NO. 309:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

SYGATAAFLS RSEASYFRTD CETGFRFLPS WTRGQGCAPS ACLPSRSQTI PTLAGLEGFD 60  
 QSGSCSDQGG GSWQGRPPFF FCLLSSLDGV GLSFGEDSL SWNWSQGRV QRQGGQKKVR120  
 V 121

## (2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 249 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

SEQGAKSADS VAAQPRPVPA EGMNHQQMSL FSKKRKGLVQ SRGLGSVLMF QPLRPAFLSR 64  
 RPFQQLQGGM ANVWFQCGGR LGWVWAARLV TLGGRSFFAF RDKLQRAAEY SESGLPRLGA120  
 VVQELVAQPI ATLATGHLQG FRSIVLRTLQ HAVGVNGLGE RRPWRRVCIL RAAGEQLIAT180  
 LGTHVNARFK VILENLAPEE AAEHGGATGT AARLPLPTDQ RLPTRRPPVP ASTSPPLPRT240  
 NRSPEGESR 249

## (2) INFORMATION ON SEQ ID NO. 311:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 204 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

LGSSNIFVNL TVRFCILGKE SFYDTFHTVA DMMYFCQMLA VVETINAAG VTTSPVLPSL 60

IQLLGRNFIL FIIFGTMEEM QNKAVVFEVF YLWSAIEIFR YSFYMLTCID MDWKVLTWLR120  
 YTLWIPLYPL GCIAEAVSVI QSPIFNETG RFSFTLPYPV KIKVRFSFFL QIYLMIFLGI180  
 LYINFRLHYK QRRRRYGQKK KXIH 204

## (2) INFORMATION ON SEQ ID NO. 312:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 155 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

RISGCSPRSS CCFQCPTADR FKKPTEQQQN EVFLRSIQKC TVPPLTRTST QVNGLSQCRR 60  
WKAAIFYVCA QPYSLEVCLA YSNISLSKA VHCYCQFDLH TVFPLDPCYH LDLVCVCVYV120  
CLCVCGLVWF ETGSCTVTGP CSAVAQSRLT AALT 155

## (2) INFORMATION ON SEQ ID NO. 313:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 70 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AVMDQVMQFV EPSRQFVKDS IRLVKRCTKP DRKEFQKIAM ATAIGFAIMG FIGFFVKLIH60  
IPINNIIVGG 70

## (2) INFORMATION ON SEQ ID NO. 314:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 112 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

FRNRKHLERK KKNPQNIQAN LYSVSFSPHP TCSPISKMKM SLPKCIQPPT MMLLIGIWIN 60  
 FTKKPMNPPI ANPIAVAMAI FWNSFLSGLV HLLTSRMESF TNCRLGSTNC IT 112

## (2) INFORMATION ON SEQ ID NO. 315:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 110 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

## (vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

DEKLSSKMYs ATNNDVINRN MDQFHKEANE SHYSKSYCCC HGNLLEFFSI RFSASFNQPN 60  
 GVLYKLPTWL NKLHYLIHDC LPNRHLKCQG HVALELADGG PPEPESGFLP 110

## (2) INFORMATION ON SEQ ID NO. 316:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 113 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

## (vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

GSSEGSYSsQ TETCPLTPSL VTGSMFAQNF LRGLSLQKSN LLPECCCLASE NLTLsFFPSVN 60  
 GHRcVAQGSSE TSesRAQWHG VALWVRKVIG QLYCKRANKYV VQFCCKQVCS VVL 113

## (2) INFORMATION ON SEQ ID NO. 317:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

GKRGQLWSLN LLAPCAGYKT RWSKIALTP NPNVQDLGA TQPVVWCWF PFFVCLLVSK 60  
 IALLGTAWKV QAFLLARSL ASSPCLHSVP KEDFCSTLWS 100

## (2) INFORMATION ON SEQ ID NO. 318:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 101 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

SQIISNLVDN YSIQELMFSE TVINRIFTSG LAGRLGGRKG RVEGWVAHQN GDEPGKTTML 60  
 LFLYPLKPIS RVLNDAFFVC FLIGSQISFS IKNWGYPKE T 101

## (2) INFORMATION ON SEQ ID NO. 319:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 368 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

WWRLNKSAS VRQQAADLIS RTAVVMKTCQ EEKLMGHLGV VLYEYLGEED PEVLGSILGA 60  
LKAIVNVIGM HKMTPPIKDL LPRLTPILKN RHEKVQENCI DLVGRIADRG AEYVSAREWM120  
RICFELLELL KAHKKAIRRA TVNTFGYIAK AIGPHDVLAT LLNNLKVQER QNRVCTTVAIL80  
AIVAEATCSFF TVLFAALMNEY RVPELNVQNG VLKSLSLFE YIGEMGKDYI YAVTFLLEDA240  
LMDRDLVHRQ TASAVVQHMS LGVYGFQCED SLNHLLNVVW PNVFETSPHV IQAVMGALEG300  
LRVAIGPCRM LQYCLQGLFH PARKVRDVVW KIYNSIYIGS QDALIAHYPR IYNDDKNHLI360  
IRLMNLGL 368

(2) INFORMATION ON SEQ ID NO. 320:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 121 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

YPFFTLQQRN RVFDISSYVK EMLQNVNCFK LKLEPLKRPY IYLIVYIMFN ICQSILQVCS 60  
FISIKYGYVY AQLLKWYICV YICTPNNIVC TFCFLYCICA GFFRLYQCNL CLLRYVQKMS120  
I 121

(2) INFORMATION ON SEQ ID NO. 321:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 114 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

FFFFFFFF HSNVYFFFF FFFFFGKNVI YLHCFHSSTV VLGLNISITL LPPIYILLEY 60  
 YYKYNIQFKK TYGETQLMFF SPLYALLSII RLQWKFIWTF SVHILAGRDT TDKA 114

(2) INFORMATION ON SEQ ID NO. 322:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 597 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

EKCGYQIQKG YSKLKIYNCE LENVAEFEGL TDFSDFKLY RGKSDENEDP SVVGEFKGSF 60  
 RIYELPDDPS VPAPPRQFRE LPDSVPQECT VRIYIVRGLE LQFQDNNGLC DPYIKITLGK120  
 KVIEDRDHYI PNTLNPVFEGR MYELSCYLPO EKDLKISYVD YDTFTTRDEKV GETIIDLENR180  
 FLSRFGSHCG IPPEYCVSGV NTRWDQLRPT QLLQNVAREK GFPQPILED GSRIYGGGRD240  
 YSLDEFEANK ILHQHLGAPE ERLALHILRT QGLVPEHVET RTLHSTFQPN ISQGKLQMWV300  
 DVFPKSLGPP GPPFNITPRK AKKYLRVII WNTKDVLDE KSITGEEMSD IYVKGWIPGN360  
 EENKQKTDVH YRSLDGEENF NWRVFPFDY LPAEQLCIVA KKEHFWSDIQ TEFRIPPRLI420  
 IQIWDNDKFS LDDYLGFLLEL DLRHTIIPAK SPEKCRDLM PDLKAMNPLK AKTASLFEQK480  
 SMKGWPCYA EKDGARVMAG KVEMTLEILN EKEADERPAG KGRDEPNMNP KLDLPNRPET540  
 SFLWFTNPCK TMKFIVWRRF KWVIIGLLFL LILLLEVAVL LYSLPNYLSM KIVKPNV 597

(2) INFORMATION ON SEQ ID NO. 323:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 76 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

IRRDKAYLTF KWRDDENPLI QSFRTKRQSS DKSMTWMKCP TGALDIFNFC DYVKEVDFD60

NGAEANISKR NPNFFP

76

## (2) INFORMATION ON SEQ ID NO. 324:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 90 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

FFLYSFSSDN HDFSFKTIY LAFVSGGELA \*SILKPAIIV NLRTGLSWGSG EGKELFEQMC60  
VGGTGFHPTA KLVLLLEISFY NTKISLCQRF 90

## (2) INFORMATION ON SEQ ID NO. 325:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 60 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

TRSLLYFHMV LILWEEVGIP FTVNGFCSII CKVHLFHIIA EIKDVQGPCR AFHPCHTLIR60

## (2) INFORMATION ON SEQ ID NO. 326:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 42 amino acids

(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

IRNEKKGCVL SVGEMELVLV VLEQDRHLVL MLWSFVIVEH RG

42

(2) INFORMATION ON SEQ ID NO. 327:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 50 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

ATCSDNRSKI FQLFNLECYV LLEPAICMYR INNFSFGQV ILRQSQWIK

50

(2) INFORMATION ON SEQ ID NO. 328:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 48 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

PKGVVVNFGA LLSQRTTASE LSACPAPTLF GPVPSHLLIR HSLSSHSL

48

(2) INFORMATION ON SEQ ID NO. 329:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

ISEVAVNFSV LLLASVCLPI DTHYTNVPSK CSLHICFHCV PTGAMKCVRS PSSGGMSAAL 60  
TTAIRIVLCG IFIYINFICT VISLFICQVT ICKSYTHKLL 100

(2) INFORMATION ON SEQ ID NO. 330:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 122 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

EAQKWDCIWT KNYKKVQSLV SRMQALALGD GSSLENAAAD SLFQRRSFER RVCYISFETV 60  
TLWRLKDLVV SCFLKITGIW RPKPFEWTDI SSKYFFIKVF EGDDELDLWL DILGFDPDYIV120  
LS 122

## (2) INFORMATION ON SEQ ID NO. 331:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 124 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

ENWASRYFQS SFTEQKVWVG HWLEGDSP TL TVTIWAATGG IVQLASRCIP HLKVCWIKAI 60  
 YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLFH SWFFFFFLLQ DLAVTQDGVQ120  
 WHDH 124

## (2) INFORMATION ON SEQ ID NO. 332:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

LNVDLLITRR LCEKIYVYIY MICRSHFFYQ ALFSLQSHSL TVCNSWFMLM IDKYPVEVTF60  
 SNYHCNDNLS HVTYCNFLAS FP 82

## (2) INFORMATION ON SEQ ID NO. 333:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

RLVKYKNSLN REKASQVFPL KVKYGTFFHN KVNDFKNLTF FRRKKKTSYE PSLVNLHLYK60  
IFPLFKKCFK KILRSHEIMP WS 82

(2) INFORMATION ON SEQ ID NO. 334:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 75 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

KLEYIMSTAN CSFCLILTDY AFPQRSSRSR IYRHIYSGSL KEKILSSIM IYHCAINQKN60  
QVRNTIKTTL KGKNF 75

(2) INFORMATION ON SEQ ID NO. 335:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 72 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

NEYCSWSTCI KQKTCQLLGA NTQNLVPVFF FFLTIVYTF LRIKFVTKSP MSFTCIYDHQ60  
MVIRATYVNA CL 72

## (2) INFORMATION ON SEQ ID NO. 336:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

THNTSTITAY RKLQSTLQAS KVHSVAQSPW RGRDLKVLMS SYFTCFLLST QCKMNFHSL60  
YFRLKIDSFL VLTLTLEGTV VPGKRSRFTV PNH 93

## (2) INFORMATION ON SEQ ID NO. 337:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 99 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

LGPRGEIEVY LAKSLAEKLY LCQYPVVRPAS MTYDDIPHLS AKIKPKQKQV ELEMAIDTLN60  
PNYCRSKGEQ IALNVDGACA DETSTYSSKL MDKQTECSS 99

## (2) INFORMATION ON SEQ ID NO. 338:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

GKSRRSACPS ASRNTCWSRR RRP RP RS AQ S APLCCGNSWG SGCRWPSQAL PSAAWA 56

(2) INFORMATION ON SEQ ID NO. 339:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 59 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

GRAEGLLVHQ LRGIRAGLVG AGPVHVQRNL LPFAAAIVGV QGVDGHLKLY LLLGLDLG 59

(2) INFORMATION ON SEQ ID NO. 340:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 157 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

QPSSLLHHC PYPYPRHLLA TPLLKPQLLA GSPAHASLIS FLASPQRASR QHGGPSQRAG 60  
TLSCPLVELG GSSGGRGLCH GSADPTNRAA EPQERGEPA GDRRLPEWG RVSLAESPGAL20  
EFCPCGSLGE WGEIPEKESS AHPKTEEAAL CPAFGSH 157

## (2) INFORMATION ON SEQ ID NO. 341:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 260 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

```

NSWCQGPQL MPASSPFLLA PKGPPGNMGG FVREPALSVA LWLSWGAALG AVACAMALLT 60
QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS RKRRAVLTQK120
QKKQHSVLHL VPINATSKDD SDVTEVMWQP ALRRGRGLQA QGYGVRIQDA GVVLLYSQVL180
EQDVTFTMQQ VVSREGQGRQ ETLFRICIRSM PSHFDRAVNS CYSAGVFHLH QGDILSVIIP240
RARAKLNLSP HGTFLGFVKL                                     260

```

## (2) INFORMATION ON SEQ ID NO. 342:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 201 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

```

TPASWIRTPY PWACRPLPRL RAGCHITSVT SESSLEVALM GTRCRTECCF FCFWVSTALL 60
FRDLSPLSQA SRASELCSGR LCQGYPSPFW EGPPVPCSR L TSLRLC SSV CNVSRAMAQAL20
TAPRAAPQLN QRATESAGSL TGPPMLPGGP LGASKKGDEA GMSWGPCQQL WFQEWGSKV180
AGRVVRVAVV QKGRRLRKE K                                     201

```

## (2) INFORMATION ON SEQ ID NO. 343:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 165 amino acids
- (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

GRRSRMEIPV FVQFSWLRRA SAPLPGLSAP GRLFDQRFGE GLLEAELAAL CPTTLAPYYL 60  
RAPSVALPVA QVPTDPGHFS VLLDVKHESP ESIYKVVGE HVEVHARHEE RPDEHGEVAR120  
EFHRRYRLPP GVDPAAVTSA LSPEGVLSIQ AAPASQAAPP PAAAK 165

## (2) INFORMATION ON SEQ ID NO. 344:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 116 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

TALAAQASQ AQSPHPNVL DCTDLPLQTI QAWFPRPOPS PATRQSTTAP SSFFSAVKPQ 60  
PATPDSGTLF RLPQLDTRF TRTENTKLYR LSHPNLRLC TDVLGLPNS NQTFSF 116

## (2) INFORMATION ON SEQ ID NO. 345:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 111 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

DIRAESGEVG VGESVQFGVG CSSWPGVQEL GQSKKGSRVW CGWLGFHGRK WAGGGSCRLS 60  
 GCRGRIGSWE PGLDGLEWEV CAVQDVWVGW GLCLTGLGLG QGCLHNNLVS K 111

## (2) INFORMATION ON SEQ ID NO. 346:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 53 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

RTEEEKKKKE KNQQFQLFTP KCWSFYVKGR IPGYGHGVYK YVGRFSANSE PTV 53

## (2) INFORMATION ON SEQ ID NO. 347:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 51 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

NELKWTNRAE LSVGWQSWKP AFPASHQLNE VMSIQLRLF FRNNHAFLNP N 51

## (2) INFORMATION ON SEQ ID NO. 348:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 150 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLDFVL VLALFLIFFY 60  
 YESPGRRGDS GSWPGPGRQV ALEMGKCLCR GAELSLCFST FPLLLPLHTP VAGRNLGFPPE120  
 SLGVPPFLPH FGGTPRAEGL FLLLESFWAV 150

## (2) INFORMATION ON SEQ ID NO. 349:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 131 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

RSFLTRSVIK LPKRKRTRGET SPGPWAFLEPG GVRRVGPPSF QGSRGSFQPR GCEGEGVEEK 60  
 RRNRERAQRL DDTFFSPGP PAVLAQASSH CHLCVQEIHN KKKSKTKPKP KQNPKGKDLG120  
 QWNEEEGRRG R 131

## (2) INFORMATION ON SEQ ID NO. 350:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 151 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

RKKGETEREL SASTQTLSHL QGHLPSWFRP APTVISASRR FLIKKNQKQS QNQNKIQKEK 60  
 TWGNGMRKRG GEEGRAGLW MHSNRARGLG RKIPQRPAAC VALARHVVEG GRLPHPVEI120  
 LVAGLLGGVK FVSDRQAGKG LGDGGGGRER V 151

(2) INFORMATION ON SEQ ID NO. 351:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 108 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

TLTAHEGRGG KCTEEGDASQ QEGCTLGSDP ICLSESQVSE EQEEMGGQSS AAQATASVNA 60  
 EEIKVARIHE CQWVVEDAPN PDVLLSHKDD VKEGEGGQES FPPELPSEE 108

(2) INFORMATION ON SEQ ID NO. 352:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

KFFGNSLHAT PKCTPITLWL FSEKDFSQIV PFTPLRAALG NSPDHLLPFS RHLCVTAGHP60  
 GLEHPPPTD THEYGLF 77

## (2) INFORMATION ON SEQ ID NO. 353:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 122 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

TYSIHLHSQT KLKSLKVHKK IAQLKSAEYT QNCHPTVFSV FPAILFPFPQT SSAPSHPKYA 60  
 IVFVILIKIL KQKFIVEQFM STKVCLSCSC PVICESSGFII QIKKILKNFL VTACMQPLSV120  
 PL 122

## (2) INFORMATION ON SEQ ID NO. 354:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 457 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

PVCEPLSCGS PPSVANAVAT GEAHTYESEV KLRCLEGYTM DTDITDTFTCQ KDGRWFFPERI 60  
 SCSPKKCPLP ENITHILVHG DDFSVNRQVS VSCAEGYTFE GVNISVCQLD GTWEPPFSDEL120  
 SCSPVSCGKP ESPEHGFVVG SKYTFESTII YQCEPGYELE GNRERVQCEN RQWSGGVAIC180  
 KETACETPLE FLNGKADIEN RTTGPNVVYS CNRGYSLEGP SEAHCTENGT WSHPVPLCKP240  
 NPCPVFFVIP ENALLSEKEF YVDQNVSIKC REGFLLQGHG IITCNPDETW TQTSACKCEKI300  
 SCGPFAHVEN AIARGVHYQY GDMITYSCYS GYMLEGFLRS VCLENGTWTW PPICRAVCRF360  
 PCQNGGICQR PNACSCPEGW MGRLCCEPIC ILPCLNGGRC VAPYQCDCPP GWTGSRCHTA420  
 VCQSPCLNGG KCVRPNRCHC LSSWTGHNCS RKRTGF 457

## (2) INFORMATION ON SEQ ID NO. 355:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 210 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

GVRAASKEIE ELRRHREGT SRAVTGEGPA AGRMTVPKQT QTPOLLPEAL EAQVLPREFQ 60  
RVLQVQAQVQ SQTQPRIPST DTQVQPKLQK QAQTQTSPEH LVLQKQVQV QLQQAEPQK120  
QVQFQVQQA HSQGPQVQL QQEAEPKQV QPQVQQAHF TAPRAGAAAA EEAGPDTDFS180  
TGAHTGHSQA SRHRELLPGA VFSFRPPGAG 210

## (2) INFORMATION ON SEQ ID NO. 356:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 292 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

GRAGRATMF SQQQQQQLQQ QQQQLQQQLQ QQLQQQLQQ QLLQLQLQLL QQSPPQARCH 60  
GVSGGGPPQPF QQPLNLQGT NSASLLNGSM RQRALLQLL QGLDQFAMPP ATYDTAGLTM120  
PTATLGNLRG YGMASPLAA PSLTPPQLAT PNLQQFFPQA TRQSLLGPPP VGVPMNPSQF180  
NLSGRNPQKQ ARTSSSTTPN RKDSSSQTPM VEDKSDPPEG SEEAEPKMD TPEDQDLPC240  
FEDIAEKRT PAPEPEPCEA SELPAKRLRS SEEPTEKEPP GQLQVKAQV AG 292

## (2) INFORMATION ON SEQ ID NO. 357:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 169 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

PRRLPSVAVG MVRPAVSIVA GGIANWSSPC NCCKSKALCR MEPLRREAEI VPWRFRRSGCC 60  
GCCGGPPLTP WQRACGGDCW SSCWSCSNCC CCNCCWSCC CCNCWSCC CCNCCCCCWL120  
NMVARLPARP QRSRRFHGWA GPAAFTPRPG GSGPRAPGLP AATPGPVGS 169

(2) INFORMATION ON SEQ ID NO. 358:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 158 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

ISKTKKYCGS PSSRIRLEGG HLEMRKARGG DHVPVSHEQP RGGEDAAAE PRQRPEPELG 60  
LKRAVPGGQR PDNAKPNRDL KLQAGSOLRR RRRDLGEHAE GQLAPRDGVI IGLNPLPDVQ120  
VNDLRGALDA QLRQAAGGAL QVVHSRQLRQ APGPPEES 158

(2) INFORMATION ON SEQ ID NO. 359:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 119 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

QSLRTLNLKN KKVWLISLEP NSARGRSPGD EKGPGRGGPCA CVPRAAERRG GRCCPGAQAE 60  
ARARAGAQT S CPGGPEAGQC QAQPGPETAG WLRPEPEATG PWFPSCRGSAG PEGWGHHRP 119

## (2) INFORMATION ON SEQ ID NO. 360:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 187 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

PPEFGWDAAE TDLLLAEEGS GWRGPHGQV LGLLWRPRRL SKLPAVDHLQ SSFSLAELG 60  
 IQGATEVVHL DIRQGVKAND DIPRGQLTL CMRAKVPPSP PEVGASLQFQ VPVGLGIVRP120  
 LAPRDSSEFP QLWLWPLFGL LGSSVLPASR LLVGHRHMVP PAGLSHLQVT ALEFNSARGR180  
 STVLFCE 187

## (2) INFORMATION ON SEQ ID NO. 361:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

STILGKSRI EFFSRCPTRV GQGFQSRILN SHRIQTPGKI ALRSQLLSSL YGSRKNSTKM60  
 TGHFMSVMEM KPHLLEKPLN QNYLFS 86

## (2) INFORMATION ON SEQ ID NO. 362:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

ITKAIVFSFV FSSGYTVEVR ESLILLFGAI IKAMQPKIK HFGSSQDDMS GDRSCGSHSN60  
 NLMGPKEKTG VNVLSFYMQ ELC 83

(2) INFORMATION ON SEQ ID NO. 363:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 117 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

YKNDRSSYER HANETPSSGE ALESELSFFL MSSDAASFLI FLKTVCF CGM YICTPNYLAL 60  
 GNHSTTQRQL NKEKENFKYQ VLSNISQTS D FIKGLPANKV HPKYTG EKAR LLQGPRV 117

(2) INFORMATION ON SEQ ID NO. 364:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

SCRCFYCPMD MPLTRFWTP NSPRMTRRHS HVICIFS YQL QIVALLRLFP VQQEMERKHF60  
 SFLHTTPLDN WKYFWVITIL GYF 83

## (2) INFORMATION ON SEQ ID NO. 365:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 144 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

QYGPSRVEVE MSYRIANTLG SFLPRLAQSR QQQQNVEDAM KEMQKPLARY IDDEDLDRML 60  
 REQEREGDPM ANFIKKNKAK ENKNKKVRPR YSGPAPPNNR FNIWPGYRWD GVDRSNGFEQ120  
 KRFAFLASKK AVEELAYKWS VEDM 144

## (2) INFORMATION ON SEQ ID NO. 366:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 116 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

KPTKHRCCQH PKKYRYLNPV IRSRIFFCGQ NWHSTSCWSV WAPIISTDNC YHWISRLCP 60  
 LPQPSHPSHL RKVTYPQHSI CRQVPELPSC WQAWQSASVQ IHWICPLRPS DIQARY 116

## (2) INFORMATION ON SEQ ID NO. 367:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 160 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

SSENFPNTAA VNTPRSTGTS IQTSGLEYSS VVKGTGIQVVA GLCGLQLLAQ TTVTTGYLAA 60  
YAHYHSPATP TASGKLHILN TPFVGKFLHC LLAGKPGKAL LFKSIGSVHS VPAISRDPDIK120  
SVGRRCWTV ARSHFFILVL LGLILLDEVG HRVPLSFLFS 160

(2) INFORMATION ON SEQ ID NO. 368:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 227 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

WESMNRWYVK PLETSSSKVK AKTIVMIPDS QKLLRCELES LKSQLQAQTK AFEFLNHSVT 60  
MLEKESCLQG IKIQGLEEV L SPTGRQGEKE EHKWGMQGR QELYGALTQG LQGLEKTLRD120  
SEEMQRARTT RCLQLLAQEI RDSKKFLWEE LELVREEVTF IYQKLQAQED EISENLVNIQ180  
KMQKTQVKCR KILTKMKQQG HETAACPETE EIPQEPVARG RMTSRRN 227

(2) INFORMATION ON SEQ ID NO. 369:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 155 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

FIFSLEGSSG RAVPAAQAGG KGGALLKGG WERSWSESES ESQEGSGGLR HWCPLWPLRL 60  
 EALGQAPEHK VRLSMEFCST CTADHISLSS FWRSSFQQPL APAVSLQSPD RRLSHDPAAS120  
 SWSGFCGIGP AFSAFSECSF SSLRSHPPAL GASDR 155

## (2) INFORMATION ON SEQ ID NO. 370:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 114 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

DLILLRLELL IDEGHLLPHQ FQLLPQELLA VPDLLGQQLQ AASGAGPLHL LTVTQGLLQF 60  
 LKALGQGPIQ LLPALLHAPL VLLLLSLAAC GAQHLFKLIN LDLLQAALLL QHGH 114

## (2) INFORMATION ON SEQ ID NO. 371:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 201 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

TASTLRAVFP RPASESPFLR ARSDAEDLTA AMSSNECFKC GRSGHWAREC PTGGGRGRGM 60  
 RSRGRGQFV SSSLFDICYR CGESGHLAKD CDLQEDACYN CGRGGHIAKD CKEPKREREQ120  
 CCYNCGKPGH LARCDHAE QKCYSGGEFG HIQKDC TKVK CYRCGETGHV AINCSKTSEV180  
 NCYRCGESGH LARECTIEAT A 201

## (2) INFORMATION ON SEQ ID NO. 372:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 189 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

LATAVTVDFT CLAAVDGYMT SFTTPIALHF GAVFLNVSEF STRIAFLLIC MVAVTSQMAW 60  
 FATVVAALLS LSLGLLAVLG NVATSTAVIA GILLKITILG KMTRLTTAIT NIWKRRGNKL120  
 ETSATASHST TTAATSRITP GPVARSTLE ALIAARGCSQ IFRVGAGPQR RRLGRRPGED180  
 GSQGRGCLF 189

## (2) INFORMATION ON SEQ ID NO. 373:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 316 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

GGDPVVSSTY RSVGCSEQQK PASSDVVLPA TMSYTGFEVQG SETTLQSTYS DTSAQPTCDY 60  
 GYGTWNSGTN RGYEGYGYGY GYGQDNTNY GYGMATSHSW EMPSSDTNAN TSASGSASAD120  
 SVLSRINQRL DMVPHLETDM MQGGVYVSGG ERYDSYESCD SRAVLSEDL YRSGDYSEL180  
 DPEMEMAYEG QYDAYRDQFR MRGNDTFGPR AQGWARDARS GRPMAAGYGR MWEDPMGARG240  
 QCMSGASRLA LPLLPEHPR VRHVEGACEV GAPSRASRF GFRVWQWHEA DEGLGRRPGF300  
 QPICEPRRRR ESRAAF 316

## (2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 200 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

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IPAAALLTGS I RMPPCFLFFF LVRKSAVVVF FVVRPHLLHA IAKPENQNGK PFGKAPQFRM 60
PLEHAVLGDD VLGEEGGQAE RHQTCGTGPG PWGLPTCAHS LRPLAGRS GH PGPSVPVWDR120
RCRCHACGTG RGRHRIGPHR PFPSQGQARC SHSLTGTGRA HSGRPSSRRT HKSHTFLHLS180
RTRLASCLS PNAAPYLSAG                                     200
  
```

## (2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 218 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```

STSHDCVPQA DAAAYSRTAD GETEARGGRG GADLPASPS PRLAPWPV RSTRGARRRR 60
TARGQAGSSS AMAAQRLGKR VLSKLQSPSR ARGPGGSPGG LQKRHARVTV KYDRRELQRR120
LDVERKWIDGR LEELYRGMEA DMPDEINIDE LLELESEER SRKIQGLLS CGKPVDFIQ180
ELLAKLQGLH RQPGLRQPSF SHDGLSLFLQ DRARTARF                                     218
  
```



## (2) INFORMATION ON SEQ ID NO. 376:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

NQLKLLKQQAG SFSQEGCKGE NILSFLQGN HCPGVPSAGR HNLSKVQGM LARKGGILDCC 60  
 LLSEPSPTPQ PASWCLFSSK LSLPNLSSSE GKRESVPGFS RVGERTGKGT DI 112

## (2) INFORMATION ON SEQ ID NO. 377:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

VRPEHSLMVL SLDTPTSYLQ FSRRRASGTL GCKPNLGSMT ALNPNSQRRS ECIFHHAAAG60  
 CWRPFCVFSQ PSEITSFLLVA VTNSWTTMK LIYFFI 96

## (2) INFORMATION ON SEQ ID NO. 378:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 145 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

SNRLVASPKK DARVKTFFPS FCREIIALVC QPVGTTFFQK FKGCWLEKEV FWIAASSQNP 60  
LLPHSLPPGV FFPNSLYLT SLHQKASGNL FRVSVWEKGG QAKAQIFRRE SSYFWPLHVP120  
YSGIVGPDOW HSDSQLNFW E NIRGS 145

(2) INFORMATION ON SEQ ID NO. 379:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 429 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

RQFEITSISV DVWHILEFDY SRLPKQSIGQ FHEGDAYVVK WKFMVSTAVG SRQKGEHSVR 60  
AAGKEKCVYF FWQGRHSTVS EKGTSAIMTV ELDEERGAQV QVLQCKEPPC FLQCFQGGMV120  
VHSGRREEEE ENVQSEWRLY CVRGEVPVEG NLEEVACHCS SLRSRTSMVV LNVNKALIYL180  
WHGCKAQAH T KEVGRTAANK IKEQCPLAEG LHSSSKVTIH ECDEGSEPLG FWDALGRRDR240  
KAYDCMLQDP GSFNFAPRLF ILSSSSGDFA ATEFVYPARA PSVVSSMPFL QEDLYSAPQP300  
ALFLVDNHHE VYLWQGWPI ENKITGSARI RWASDRKSAM ETVLQYCKGK NLKKPAPKSY360  
LIHAGLEPLT FTMNFFSWEH REDIAEITEM DTEVSNQITL VEDVLAKLCK TIYPLADLLA420  
RPLFEGSIL 429

(2) INFORMATION ON SEQ ID NO. 380:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 169 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

DVFHEGDLIG NFRVHLCOLS DVLSVLPAGK HIGECQGLQT SVDKVRLGGW FLEIFSFAVL 60  
 ESHLHRTLEV GGPADAGGTS DLVLDGPPAL PEVHLVVIWN KEKCWLGRAV QIFLQEGHGT120  
 DHRGSGSRVH KLCGCKIPRG AAEDQAGRE VKTSRILKHA IVGFVPS 169

(2) INFORMATION ON SEQ ID NO. 381:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 234 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

GIPSEWLGA FITLVYCDFA ATMQSCFQGT LFLDLVRS GP SDLLRVGLGF ASVPQVDEGL 60  
 VDVKHHHGSS GPQAATVTGH FQIIPFHGL STHAVQPPLT LHIFFLFPP PRVHHHPPE120  
 TLQETGGLLS LENLDLGPFF LVQLHRHQRR RALLTHGGVF ALPEEVDALL FAGCPHRVLS180  
 LLATSHCRAH HELPLDHIGI PLMELPDALF GEPAIVEFQD VPDHGNAGD LKLF 234

(2) INFORMATION ON SEQ ID NO. 382:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 81 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

RLFAPLRTSW AVVIFGARVA LCFYKIMTYV TCLHVCLLVE FLNSQLTNHR KYFSLSYGF60  
 FTGLRGFSEY LWPQQTQFP S 81

## (2) INFORMATION ON SEQ ID NO. 383:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

IVNRTTACTL FEVNLEWKAR DYTLEFKIDIC GAHTIYEIVP SKKEKKKIRR SNLEQHCLIK60  
 A 61

## (2) INFORMATION ON SEQ ID NO. 384:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 56 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

PPDFFFLFFR GYFYICVSP TNVYFKKSIV PGLPFQIHLK ESTCSPVYN LIEMRK 56

## (2) INFORMATION ON SEQ ID NO. 385:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 139 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

LOSSHCCSCS TALFRTQTTA AAVPRMVIRV YIASSSGSTA IKKKQQDVLG FLEANKIGFE 60  
EKDIAANEEN RKWMRENVPE NSRPATGYPL PPQIFNESQY RGDYDAFFEA RENNAVYAFLL20  
GLTAPPGSKE AEVQAKQQA 139

(2) INFORMATION ON SEQ ID NO. 386:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

ETKHILLFLL NRCRARGRCN IYTDHHPGNS GCGCLGPEKG CGAAAAMAGI QLGAETAVGR60  
EGWGKVEGEL ARAPFFPLAA STELSKRCSS SPKPR 95

(2) INFORMATION ON SEQ ID NO. 387:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 96 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

FCIRFECLHV KTQLIYYFNI KPISFEAKLI LLFYKSNQDS FFRMLKAQCL RFMLAALLAL60  
LLPLNQVGLS SLRRHTLHYF LWLQRRHSP RDTGFH 96

## (2) INFORMATION ON SEQ ID NO. 388:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 221 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

```

FIMLNIIILIK FSSFSIRCAI LSSVCLNEAI TFAFLQVFL WNMDKYTMIR KLEGHHHDVV 60
ACDFSPDGAL LATASYDTRV YIWDPHNGDI LMEFGHLFPP PTPIFAGGAN DRWVRSVSFS120
HDGLHVASLA DDKMVRFWRI DEDYPVQVAP LSNGLCCAFS TDGSVLAAGT HDGSVYFWAT180
PRQVPSLQHL CRMSIRRVMP TQEVQELPIP SKLLEFLSYR I 221

```

## (2) INFORMATION ON SEQ ID NO. 389:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 118 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

```

KGGATCPESP QDRKRRGNLD MEKLYSENEG MASNQGMEN EEQPQDERKP EVTCTLEDKK 60
LENEGKTENK GKTGDEMLK DKGKPESEGE AKEGKSERE ESEMEEVERE GTRGRGSG 118

```

## (2) INFORMATION ON SEQ ID NO. 390:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 138 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

RFPYLGFPPLS RPPPSLTLPPL SLTFLLPLP HSLAFLYPLT FPHLLFCPCF LSFFRFLTSC 60  
 LPEYKLLLAF SRLVAVLHFP SFLGLKPFLH FHCVRVPCRD FPSFSCPAGI LDRLLLLFSF120  
 AERWEQQTRR PGRSWTKN 138

(2) INFORMATION ON SEQ ID NO. 391:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3218 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

GCGACCACGA GCTGGTGCAT CCATCAGTAC CCTTGCCGGA CTTTCCCTTA AAGAAGGAGA 60  
 GGATCAGAAA GAGATAAAGA TTGAGCCAGC TCAGGCTGTG GATGAAGTGG AACCTCTACC 120  
 TGAAGACTAT TATACAAGAG CAGTAAATTT AACAGAGGTA ACAACCTCTC AGCAGCGTCT 180  
 GTTACAGCCT GACTTCCAGC CAGTCTGTGC TTCACAGCTC TATCCTCGCC ACAAACTCT 240  
 TCTGATCAAA CGGTCCCTGC GCTGCCGTAA ATGTGAACAT AATTGTGAGCA AGCCAGAATT 300  
 TAACCCACAG TCAATCAATT TCAAAATCCA GCTGGTGCCT GTCAATTATA TTCGAGAAGT 360  
 GAGAATCATG TCAATTCCCA ACCTTGCCTA CATGAAGGAG AGCCAGGTCC TCCTGACTCT 420  
 TACAAATCCA GTTGAGAACC TCACCCATGT GACTCTCTTC GAGTGTGAGG AGGGGGAGCC 480  
 TGATGATATC AACAGCTGCT CTAAGTGGT GGTGCCCTCC AAAGAGCTCG TTGTAGTCTG 540  
 CAAGGATGCA GCAGCAGAGT ACGATGAGTT GGCAGAACCT CAAGACTTTC AGGACGATCC 600  
 TGACATTATA GCCTTCAGAA AGGCCAACAA AGTGGGTATT TTCATCAAAG TTACACCACA 660  
 GCGTGAGGAG GGTGAAGTGA CCGTGTGCTT CAAGATGAAG CATGATTTTA AAAACCTGGC 720  
 AGCCCCCATT CGCCCCATTG AAGAAAGTGA CCAGGGAACA GAAGTCATCT GGCTCACCCA 780  
 GCATGTGGAA CTTAGCTTGG GCCCACTTCT TCCTTAAAGG GTTCCACTGG AGGGCAGATC 840  
 CCAAAGGACA GTATCACCGT AAACCTGCGT TAAAAATGTG AAGCTGCTGC TTCATTAGGC 900  
 CTTGTTTATA ACGATGTACC CATGCACTAC GGAATTCTAT TGCTAAGAAA GTGGGAGCAT 960  
 AGGCAAGGCA TTGGGAACAC AGGGTAGCTG CTGTCTCACC CTGTTTGACA1020  
 CCAGTAAGTC TGTGTCTCCC TCACTGAACC CTGACGTTAG AGTAACAGCA GCATAATTCC1080  
 ATCCTAGGAA AGGGGATGAG TGTCTCTTGG AATGGCACTG TATTTACCAT CTGAGAAACT1140  
 CTGTACTGTC TCTTGATCTG ATCTCACTAA GGATCACAAT GTCACAGATG AAACTTAAAT1200  
 GATAACCCAA AGGTAGACCT GCTGTTAATG ATCCAGCATT GGTCAACAATG TACCAACTGC1260  
 TTCTGCGATT CGGTTAATA TCACTAACA GTCTAAACCA TATCCCTTCA TTGCCATPAT1320  
 GGCTGCCATT TTGCCATAGA TTTCCATATA ACTGAAACAC TGAATTGTCA CTTTATCTTT1380  
 AGTATCATGA TGATTGGAAA AACCTGTGAA GTTGTTAAGG CACTCTCATT TCGCCTCTTT1440  
 TTCTAAGTGA ATACAGGACA CGTATTAGTT GTTCTTAANN NNNNNNNNNN NNNNNNNNN1500  
 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN GGTAGCAGAT1560  
 TCCATTGCTT TTCAATATTG CCACAATACC CAGGGATTAA TGCTGCCACA GGGGGGCAAT1620  
 CTTTATTGTT CTTACTTCCT ACCCCTTCCC TGTCTGCTCT CTTTAACTCA GTTAAGTTGT1680  
 TCTGTTTGGG ACCTGGAATA GAACCCAAAG AAAACCTGAG TGGACAGGTT CATTTCTGGA1740  
 ATGCAGAAA CATTTTAAGG GCTAGATTTT TAGAATATTC TCAACTAGCA TTCTTTCGAT1800  
 TGATTGGAAG GGGAAATTA TATTATAAT CTCTTGAATC CAAAACCTGGA TATTAAAGAC1860  
 TTTCCCCCTT ACTAAGTTTA AGACTTTTGT CATGTGGTGA GTCAAAATAAG ACCATTTTGA1920  
 TTGTAAACCA TAAATAGTT CAGCAAGTAG CCCACAGTTT TGGCCTAACA GCAGACTTGC1980  
 TGTGTTCACT TGGTATCCTG GAGTTGGGTT GCTAACCTTA ATTTCTATGA TGTGTTCTAA2040  
 AATGAAACTT GATAAAGTAG ACCACGAGCT GCACCGTGTG TTCTGTAAAA GTATTGTTAG2100  
 TAAGTGCCCA AGAGACTTGA GGAATAACA GATTTTTTGT TTACCTTGGT CTGTGTTTAA2160  
 GTCTTAAAAA ATTAAGATA ACATTATAAT GTAGAATACA TTAGGACAT AGTCCTTGTA2220  
 AGCTTCCCTT GAAATGTTT TAAATATTTA GGAAGCTTTT AAAAGACAT AAATGTGACT2280  
 CTAAAGACA CTAATATGTA CTAATTGTAC AAAGGTCAAG CCAATTTTAT GAACAGTCC2340  
 TACAGAGTAA TATATGTGAT GCAGTGTAA GAGGAAATA CTATCTCTA ACATTATGGT2400  
 AATAACATT AGGCTCTTAG GAGTTGGAGC AGGGGGATGG GTAATTACAG ATTTGCAGAC2460  
 TATGAARAGA GTTTCATTTT TTTGTGACCC CACAGAGTCT CAAATTTTTC TTTTACC2520  
 TGCTAGAGCC TACTGTGAAA TCACTGCTCC ATATTGGCCA GTGGAGGAAA TGGGATAGA2580  
 TAGAGAATA GCTTCATATG GTTTACAGCT TTGCATAGAC TACACACATG TACTGCGTT2640  
 ATGGCAGGTA GCTGGTATTT ATCCCAAGAG TAATAATGTT GAAGTATGGG TCTCATCAT2700  
 CCCATACACA GAAACACAAA ACACCTTTGAT CATAAACTTT TTCTTTCAGA AGCCAAACTA2760  
 ACTTGCAGAA TAATAGAGGC ACTGGTTTAA TGTTTCTCTA AGATAGGTTT TAGTGTAAAG2820  
 TAGTTATCTG TGTGTTCTGA GAAATGATTC AATACCTGCA CCGTGTGAAT TAGGAATTGT2880  
 ATTTGTTGGC TTTTATTAT TAGATGAGGT GCAAAATTTT TAATGCTAGT CAGTATGCAC2940  
 CACCCACAGG AAGTTAGATC CCATTAGCAC TTGAAACTAC AGCTTTGGAA ATTTAGGCTA3000  
 AGTTAATTTG GATTTGTTAC TACTGACCTT TCTTTTGTGT TGAAGTGGCT3060  
 ATCAGCATAA TGAGCTAAGT GTCATGCATA TTTGTGAAGA AACACCCCTT TTGGTCCCTT3120  
 TTGGGACAGA GAGGTACTCC TTGATCTTTA TGAATGACAG GTTACTGTGT TGCCTTTATG3180  
 CTTAACTTAA TGTAGTAAAA TAAAGCAGAC AAAGCTTG 3218

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## (2) INFORMATION ON SEQ ID NO. 392:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 750 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

```

GTGAGGGACA GATGGACAGA ATGCAGAGGT ACATAGATGA GCTGAGGCTG ATCCAGCTCC 60
CCTGAAATTC AGAGTGTTAA CTTTGTAGAC CCGCACAAAT CTCTTGGTGC TATCTAGCCAL20
TTACCCCAT TTTTTTTTAA AAGGCCATCT GAAATTCAT TTGTCATGCT GGGAGACATT180
TTGGATATGA TGCAGGAAAT CTCTTCCTGG AGTCAAAAGT TCCCAAGAGG TCCTGTATTT240
TTAAGAAATG GAATTTATTT AAATAATATT TAAGCTTGTG CCCATGTTGG CCGGGCAACT300
TTTTTCATG GTGCTTATTA GAAGAAGTTT TTTTCATCTG TCATTTTAAG AAAATAAAAC360
TGGAAATGA ATATGGGTGG CATGATTGTA CCTTTTAGT TCTCTTATTT TTCTACTCCT420
CTGTCCTCTC ATAACATATG CATACTATTA GATGCTGGTC CACTGAATGC TGAGATGATC480
TGTTTTTTGG GGTTTTTTTT TTTTAAAGAA TATTTTCACT GGTTTTCTGT GACTCTCTAA540
ACACTTCATC GAAACTAGGA AGACTGAATT ATGAGGGAAA CTATTGGGGA TTAGTGGCCA600
GAAACGATGA AATCTTATAG ATCTTTTAC AGTTTCTCTG TTAGGGGGA GCCTAGGACT660
GATATCCAG TTTCTTCCAT ATCCAAGCTT CATTGGGGGA CCCCATTG GCTTTAACAG720
GTGACCCGGC CCTCTTACC GGGCTTCCAG

```

750

## (2) INFORMATION ON SEQ ID NO. 393:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 546 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

CACGAGGAGG CCGGGAGTGG AACCCCTCT TTTGAGAAGG TTGCCTGACT CAGAGACACA 60  
 GAAACGGGTC CAGGGATGGG GAGAGATGTG GAGTGAGGGA AGGTTTGCAT TTGAGAAAGG120  
 AAGTTTCGAGA ACACACTGGG ACATTGTAAC ACATTTGAAC CATCTTCTGA TAGAAAGGTG180  
 TTGGCCTCCT AATAATGGGA GGTGAGGGCC AGGTCCCTCGG GCATAGGGAG AGGGTCCGGA240  
 GAATGCTGCA GACCCCTGCC CACTGCCAC GGTCTCCGCT CCCTGCACCT GCCTCTGATG300  
 GTGCAGCTCT GATTCCGTGT CTCTCCTCAT TGCAGATTTA TGAAGGTGCC TACCATGTTG360  
 TCCACAAGGA GCTTCCTGAA GTCACCAACT CCGTCTTCCA TGAATAAAC ATGGGGTCT420  
 CTCAAAGGAC AGCCACGGCA GGAACCTGGT CCCCACCCCTG AATGCATTGG CCGGTGCCCG480  
 GTCATGGTC TGGGGGATGC AGGCAGGGGA AGGGCAGAGA TGGCTTCTCA GATATGGCTT540

GCAAAA

546

(2) INFORMATION ON SEQ ID NO. 394:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2453 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

```

CCTGACGGGA CCAAGCGGCG GGGAGTCTGC GGTGCTGTCC TCGGCTGTGG ACCGGGCGGC 60
ACGACGGCGT GCAGGGTAAAC ATGGCGGATG CGGAAGTAAT TATTTTGCCA AAGAAACATA 120
AGAAGAAAAA GGAGCGGAAG TCATTGGCAG AAGAAGATGT AGCCGAAATA CAACACGGTG 180
AAGAATTTTT TATCAAAACCT GAATCCAAAG TTGCTAAGTT GGACACGCTCT CAGTGGCCCC 240
TTTTGTCTAAA GAATTTTGAT AAGCTGAATG TAAGGACAAC ACACATATACA CCTCTTGAT 300
TGGTTCACAA TCCTCTGAAG AGAGAGATTG GGGACTATAT CAGGACAGGT TTCAATTAATC 360
TTGACAAGCC CTCTAAGCCC TCTCCCATG AGGTGGTAGC CTGGATTGGA CGGATACCTC 420
GGGTGGAGAA GACAGGGCAC AGTGTACTC TGGATCCCAA GGTGACTGGT TGTTTAATCG 480
TGTGCATAGA ACGAGCCACT CGCTTGTTGA AGTCACAACA GAGTGCAGGC AAGAGTATG 540
TGGGGATTGT CCGGCTGCAC AATGCTATTG AAGGGGGGAC CCAGCTTTCT AGGGCCCTAG 600
AAACTCTGAC AGGTGCCTTA TTCCAGCGAC CCCCACTTAT TGCTGCAGTA AAGAGGCAGC 660
TCCGAGTGAG GACCATCTAC GAGAGCAAAA TGATTGAATA CGATCCTGAA AGAAGATTAG 720
GAATCTTTTG GGTGAGTTGT GAGGCTGGCA CCTACATTG GACATTATGT GTGCACAGTG 780
ATCAGTCACG CGCAGCAGGT ACGTCAGATG CAGGAGCTTC GGAGGGTTCT TTCTGGAGTC 840
ATGAGTGAAA AGGACCACAT GGTGACAAAT CATGATGTGC TTGATGCTCA GTGGCTGTAT 900
GATAACCACA AGGATGAGAG TTACTGCGG CGAGTTGTTT ACCCTTTGGA AARAGCTGTT 960
ACATCTCATA AACGGCTGGT TATGAAAGAC AGTGCAGTAA ATGCCATCTG CTATGGGGCC1020
AAGATTATGC TTCCAGGTGT TCTTCGATAT GAGGACGGCA TTGAGGTCAA TCAGGAGATT1080
GTGGTTATCA CCACCAAAAG AGAAGCAATC TGCATGGCTA TTGCATTAAAT GACCACAGCG1140
GTCATCTCTA CCTGCGACCA TGGTATAGTA GCCAAGATCA AGAGAGTGAT CATGGAGAGA1200
GACACTTACC CTCGGAAGTG GGGTTTAGGT CCAAAGGCAA GTCAGAAGAA GCTGATGATC1260
AAGCAGGGCC TTCTGGACAA GCATGGGAAG CCCACAGACA GCACACCTGC CACCTGGAAG1320
CAGGAGTAGT TTGACTACAG TGAGTCTGCC AAAAAAGAGG TGGTTGCTGA AGTGGTAAAA1380
GCCCCGCGAG TAGTTGCCCA AGCAGCAAAA ACTGCGAAGG GAAGCGAGGA GAGTGAGAGT1440
GAAAGTGACG AGACTCCTCC AGCAGCTCCT CAGTTGATCA AGAAGGAAAA GAAGAAGAGT1500
AAGAAGGACA AGAAGGCCAA AGCTGGTCTG GAGAGCGGGG CCGAGCCTGG AGATGGGGAC1560
AGTGATACCA CCAAGAAGAA GAAGAAGAG AAGAAGGCAA AAGAGGTAGA ATTGGTTTCT1620
GAGTAGTGAA GGCCACTTGA AGCTGGAGGA GAAACTAAAG CCTTTATTGAG AAAACATGTT1680
ATAGATCCTT TTGTTGCTGA GAGAGTGGAA CATAGTCTCT AGACAGGGTG AAGAGTTCTG1740
GCACATTTTA GCTGCTACTT TGAGACCTCG GTGATGTTAC CTGGTGTTGG CATCCCCTCT1800
TGCTCTGTTT TAAGGATATA GGTGGTGAAA GATGAAAGAG GCAGAGTTTA TCCCAATGAC1860
TTCTCTGTTT GAGTTGGGAA GCCTCACCTT CAGACCCAGT AACTGTCCGC AGCTGTCTGC1920

TAGTGGTTGT CTTAACAICG TAGTCCTAGT TTGCATTTT TAAATCCCCT CTGTTTAAAA1980
GGTTTGTAAA ACAAAAAACA AAAACTAAGT CTGCTCAGTG AAATGCTGTA GAACCCCTAAA2040
TAAGTGGTAG AAGAGTGTC ACGAATTTTG TCTCTGAATT CAGTATAACT GAGTTTGTCT2100
CATGCTGGTG TCTGGGTTAT AGGCCTGATG GGCTGGTAG TTTTCCATCT TGGTTCTGGCC2160
TAGAGGTACG TCCTTTGCAC TTCTCAAAAG CTTGTGTACA GTGCTCACCT AAATCCATCT2220
GACTACTTGT TCCTGTGCCC TCTTGTTTTA GGCTCGTTT ACTTTTAAAA AATGAAATTG2280
TTCATTGCTG GGAGAAGAAT GTTGTAATTT TTACTTATTA AAGTCAACTT GTTAAGTTT2340
TTATGTATTC CTGTTGGGTT TTCTTGTGTA TCTCATGCTA GCAGAGCAAA AATTGTAAAA2400
TATTTTGATT AAAAACTAG GGACCTTTAT GTCTATTGTT AAAAAAATAA AAT 2453

```

## (2) INFORMATION ON SEQ ID NO. 395:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2706 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

```

GGGAGGAAGG AGACTACACC TGCTTTGCTG AAAATCAGGT CGGGAAGGAC GAGATGAGAG 60
TCAGAGTCAA GGTGGTGACA GCGCCCGCCA CCATCOGGAA CAAGACTTAC TTGGCGGTTC 120
AGGTGCCCTA TGGAGACGTG GTCACTGTAG CCGTGAGGC CAAGAGAGAA CCCATGCCCA 180
AGGTGACTTG GTTGTCCTCA ACCAACAAAG TGATCCCCAC CTCCTCTGAG AAGTATCAGA 240
TATACCAAGA TGGCACTCTC CTTATTCAGA AAGCCACGCG TTCTGCACAG GGCACCTACA 300
CCTGCTTTGGT CAGGAACAGC GCGGGAGAGG ATAGGAAGAC GGTGTGGATT CACGTCAACG 360
TCCAGCCACC CAGATCAACG GGTAACCCCA ACCCCATCAC CACCGTGCAG GAGATAGCAG 420
CGGGGGGCGAG TCGGAAACTG ATTGAGTGCA AAGCTGAAGG CATCCCCACC CCGAGGGTGT 480
TATGGGCTTT TCCCGAGGGT GTGGTTCTGC CAGCTCCATA CTATGGAAC CCGATCACTG 540
TCCATGGCAA CGGTTCCCTG GACATCAGGA GTTTGAGGAA GAGCGACTCC GTCCAGCTGG 600
TATGCATGGC ACGCAACGAG GGAGGGGAGG CCAGGTTGAT CCTGCAGTCC ACTGTCTCTG 660
AGCCCATGGA GAAACCCATC TTCCACGACC CGATCAGCGA GAAGATCAGC GCCATGGCGG 720
GGCCACAACA TTCAGCCTCA ACTGCTCTGC CCGGGGGACC CCGACACCCA GCCTGGTGTG 780
GGTCCTTCCC AATGGCACCG ATCTGCAGAG TGGACAGCAG CTGCAGCGCT TCTACACCAA 840
GGCTGACGGC ATGCTACACA TTAGCGGTCT CTCCTCGGTG GACGCTGGGG CTTACCGCTG 900
CGTGCCCGCG AATGCCGCTG GCCACAGGGA GAGGCTGGTC TCCCTGAAGG TGGGACTGAA 960
GCCAGAAGCA AACAAAGCAGT ATCATAACTT GCTCAGCATC ATCAATGGTG AGACCCCTGAA1020
GCTCCCTTGC ACCCCTCCCG GGGCTGGGCA GGGACGTTTC TCCTGGACGC TCCCAATGG1080
CATGCATCTG GAGGGCCCCC AAACCCCTGG ACGCGTTTCT CTTCTGGACA ATGGCACCC1140
CAGCGTTCTG GAGGCTCTCG TGTTTGACAG GGGTACCTAT GTATGAGAGA TGGAGACGGA1200
GTACGGCCCT TCGGTACACA GCATCCCCGT GATTGTGATC GCCTATCCTC CCCGGATCAC1260
CAGCGAGCCC ACCCCGGTCA TCTACACCCG GCCCGGGAAC ACCGTGAAAC TGAACCTGCAT1320
GGCTATGGGG ATTCCCAAAG CTGACATCAC GTGGGAGTTA CCGGATAAGT CGCATCTGAA1380
GGCAGGGGTT CAGGCTCTGC TGTATGGAAA CAGATTTCCT CACCCCGAGG GATCACTGAC1440

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CATCCAGCAT GCCACACAGA GAGATGCCGG CTTCTACAAG TGCATGGCAA AAAACATTCT1500
CGGCAGTGAC TCGAAAACAA CTTACATCCA CGTCTTCTGA AATGTGGATT CCAGAATGAT1560
TGCTTAGGAA CTGACAACAA AGCGGGGTTT TTAAGGGAAG CCAGGTGGG GAATAGGAGC1620
TCTTAAATTA TGTGTGCACAG TGCATGGTGG CCTCTGGTGG GTTTCAGTT GAGGTTGATC1680
TTGATCTACA ATTGTTGGGA AAAGGAAGCA ATGCAGACAC GAGAAGGAGG GCTCAGCCTT1740
GCTGAGACAC TTTCTTTTGT GTTTACATCA TGCCAGGGGC TTCATTCAGG GTGCTGTGTC1800
TCTGACTGCA ATTCTTTCTT TTTTGCAAAAT GCCACTCGAC TGCCCTTCATA AGCGTCCATA1860
GGATATCTGA GGAACATTCA TCAAAAATTA GCCATAGACA TGAACAACAC CTCACTACCC1920
CATTGAAGAC GCATCACCTA GTTAACCTGC TGCAGTTTTT ACATGATAGA CTTTGTTCCT1980
GATTGACAAG TCATCTTTCA GTTATCTCTC TGTCACCTCA AAACCTCCAGC TTGCCAATAA2040
GGATTTAGAA CCAGAGTGAC TGATATATAT ATATATTTTA ATTCTAGATT ACATACATAC2100
AGCTACCAT TATATGAAA AAAGAAAAAC ATTTCTTCTT GGAACCTACT TTTTATATAA2160
TGTTTTATAT ATATTTTTTT TCCTTTCAAA TCAGAAGATG AGACTAGAAG GAGAAATACT2220
TTCTGTCTTA TTAATAATTAA TAAATTATTG GTCTTTACAA GACTTGGATA CATTACAGCA2280
GACATGAAAA TATAATTTTA AAAAATTTCT CTCCAACCTC CTTCAAATTC AGTCACCACT2340
TTCTGTCTTA TTAATAATTAA TAAATTATTG GTCTTTACAA GACTTGGATA CATTACAGCA2280
TATGCAAGT TTTTGTGAA AGCTGTGCTC AGAGGAGGTG AGAGGAGAGG AAGGAGAAAA2460
GTTATATTAC CTTCTCCAGG AACCTGCCAG TGGGGAAGTG TGCATATTA GATTTCCTTG2400
CTGCATCAT ACTTTACAGA ATTGAATCTA GAGTCTTCCC CGAAAAGCCC AGAAACTTCT2520
CTGCAGTATC TGGCTTGTCC ATCTGTGCTA AGTGTGCTGC TCTTCCCTCA GCCATGAGTC2580
AGTTTGTGCC CATGAATAAT ACAAGACCTG TTATTTCCAT GACTGCTTTA CTGTATTTT2640
AAGGTCAATA TACTGTACAT TTGATAATAA AATAATATTC TCCCAAAAAA AAAAAAAA2700
AAAAAA

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2706

## (2) INFORMATION ON SEQ ID NO. 396:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2242 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

CAGGCCGGTT CCGGCGAAGT TAAACCCCTCG GAGCTGGCCT CGGACTGCTG GGGCGTTACC 60  
 CCTTCGGGCA CCCCCTGCTGA CCATGGCGAGT GTTTCATGAC GAGGTGGGAAA TCGAGGACTT 120  
 CCAATATGAC GAGGACTCGG AGACGTATTT CTATCCCTGC CCATGTGGAG ATAACCTTCTC 180  
 CATCACCAAG GAAGATTTCG AGAATGGGGA AGACGTGGCA ACGTGTCCTA GCTGCTCTCT 240  
 CATTATAAAA GTGATTTATG ACAAAGATCA GTTTGTGTGT GGAGAAAACAG TCCGAGCCCC 300  
 TTCAGCCAAC AAAGAATTAG TTAATGCTG AAGAAGCCTT CAGGAATCCA AATCCTGAAC 360  
 ATTTGGGAATG AGCCCGAGTA GAAATATGCA ATGCAAGACT ACTGGCTTCA CAGAGACAAC 420  
 CATTTATGAT TTGCTGTTCT GTAAGAGTGT GGATTCCTTC TATCAACTGC TGATATCATC 480  
 TTCAGGAAGC AAGTCCATAA CATGACATAT CTGGAATTTG TGCTTAGAAC CTTAAATTTG 540  
 AAGCATTCCT AATTATGCAT CTTAAATTTAA AAGAAGATAA TTTCAAAACA GTGCTTTCTT 600

TCCCTTGGTT TCATCATTTT CATATCTTAA ACCAAATTAC TTCGGTATCT GACACACGCA 660  
 TCATCTACCT CAGTCATTAG GATTTCTTAA TAAAAAGAG ATTGTATTTT TGACTTGGTT 720  
 ATTAAGATTA TTAATAATTAG CCCTTCCTTT GAAATATGAC ATCAGCTTTG CTGTTCTAAA 780  
 TTTAAATTA GTTGCTTCAT CAGTACCACA CTTCAGTTT CTATACCAG CCAGTCTCCT 840  
 CAGTTTTCCT ATTAGAATGG ACATGTTCTG TTCAGCGTGT CATTTCGTGA ATGCTTCATG 900  
 CAGAGAGTTT GGTTCATAGTA TTAAGAGAGAA AATACAGTGA GGTCAACAAT TCTCCAGAGC 960  
 TAAAGTTTAG TGAACAAGAA AGAAAGTCCA AAATGAAGTG ATGAAAAGAT GAGGACTTTT1020  
 CTTATATTC GCATATTCCT TGGAAGTCAG GACAAGATGA AAAGAAAAAC ATCCAAAAGA1080  
 AGTGAATTT GTGACAGAAT GAGAGGAGCA AAGCATACCA GTGTAGTAAG TGAATGTTT1140  
 GATGACTTT GCCAGGTCAG AGCAAGTAAT ATTTCTGTAT CTGAGTTTTT GTTTGTGTTT1200  
 TGATAAGGCT AATGAAATTG CATTCAGGCT AGGGGTTAAC GTCAAAATTC CATGGCTGGT1260  
 AGCTGTGCTT TTGGCATACT ACAGTGTGTT GTCACTACTA CAAGGTAAAG CATCTACAGC1320  
 GGAGAATGAG CTTGAAAATG AGAGACCTAT TGTGAATAAA TATGCCCATG AGAGCATATT1380  
 TAATAAGCCT CTATAACATG CAGCCAAACC AGACATTCAC TCCTGCAGAG AAATGTTGCC1440  
 CTGGAGAAAA AGAGATATAT AAAGATAGGC TATCACCCCT CTTTTGCTGC AGTACTAAGC1500  
 ATAGCAAGAA ATTAGAATCA TTTACATTGG AAATTTGAAA ATTCCTCTTA TATACACAAC1560  
 TTTACTGTGT ATAAATAAAA AATATTTATT AATGCAGTGA TGTCCGTCAG GTTGTGTTAG1620  
 GAATGGCTTC TGCAATTAGA AAAATAGCTT GCTAGAATGT AAATGTTCTG CTACTGGTAA1680  
 ATGTACTGCA CACATTCATT GGACGTTAAA ACAAGTGAGT AGCCTTTTTT ACCTGGCAGC1740  
 AGCATGGCTG TGTGAGGCA CTAGGCTGAG ACAATAAATT ACCAAAAAAT ATAATGTACC1800  
 GAGCTGAAAA TGCTCAGTAC ATTATGTGGC ATATCTGGA TGTGATGAGA AATCTCATTG1860  
 CCATTTGGGA CACTGACATC CAGAAGTAA TCCACAACCT CACTATGGTG GCATCAGCTG CAAAGCGAAA1980  
 TGCTCAGATG AACAGAGCAG AGTACTCACT CACTATGGTG GCAACATGT TAGCTCTTTC2040  
 TGAAGTGTCC CATGATCATG TTGATGGTTT TCTAGATACT GCCAACATGT TAGCTCTTTC2040  
 TGATGCTGAT GAGTTTCAAA CACGAAACAGA CACCTTGAT GTGGGTTTGC TAAGAACAATA2100  
 GRAGAACAGG AAGAAAAGTT GCCAGGTTT AAAAATCCCA GGGAAAAAAG AAGCATAAAA2160  
 AGCATTAGCA GTCACTGACT GATGATAATG CTTGCAATAA TGGGGAATGG TTTGTTTTC2220  
 TAAAAACCAA AATTATTTC TT

2242

## (2) INFORMATION ON SEQ ID NO. 397:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1239 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

```

TAGTCATCCT ACAACATGT TTCTGTTACT TCCTAATATT AAAATAGCCA TTTTGGATTC 60
CATATTTAAA GTGCTCATTT GAGTGAAATT CAAATTAGAA AGAAAATATAT TAAAATGCGC 120
CTAACAAGAAA CCTCTCTTTC AGAATCCCTA TTCCTTGAAT CTGGGGTTTG AACTGCTTAT 180
TAAAGGCAGG CCTAAACTAA TTTGTGAGAA ATGAAGAAGT TTTAGTATAT AATTCTTTTA 240
AAAAATATCA ATTACGGCTG GGTGCGGTGG CTCAGGCCTG TAATGCCAGC ACTTTGGGAG 300

GCCAAGGCGG GTGATCACCT GAGGTCAGGA GTTCAAGACC AGCCTGGCCA ACATGGCAAA 360
ACCCTGTCTC TACTAAAAAG TAAAAAAAT TAGCCGGGCA TGGTGGCTTG TGCTTGTAGT 420
CCCACTTCAG TCTAAGTAGC TGGGACTACA GGCACGTGCC ACNAGGCCCA GCTAATGTGG 480
GTGTTTTGTT AGAGATGAGG TAGGGCCATA TTGCCCAGGC TCGTCTTGAA CACCGGGGCT 540
CAAGGAATCT GCCCATCTTC GCTCCCAAA GTTCTGAGAT AGCAGGTGTG AGTCANTCAT 600
GCCCAGCCTC CTTGAAGTTT ACTAACAAAT GGGATAACTG AGGGAAGAGA AGTGACAATT 660
CCACTCAGTC TATTAGAGGT CTGGATATRA GGTAGNCCAC ACAATACTC TAACNTGAC 720
TTCTAACCAT TCTATCTTAT TGNATTGGA GGCTGCTTC TGNCCAGATT TTTTGTGCT 780
TGAGATGATA TTTTNCGAAC CTTCTTTTCA CTACCTTTCT TACCCTTAAT GTGNCCAAGC 840
TTGAAACAGG ATTTGATTTT CTGAGCNTAC TTGTTTCGCC TTCTGTGCGT CANCCAAGTA 900
ATCTGGTTCA TCTTTNCGTN CTCATTCATG TTATTTTCAA GTGAACAAG ACATTTTGGG 960
GGNTCAAGTC TCNITTGGGN NGTTTTGTT TTTATGTATA TAAAAATGGA TTTTNGTGT 1020
CCCTTTCCNA TGTNAAGTAN CCAACTTATA TGGAACTCA CAATCATAT GTAAAGAAG 1080
AATGAAANGC CTGGTGTTAT GTACTTCAAG ATGCCTCCCT GNATGTATAG AATCCTCTT 1140
GTAAAAATAA TAATTGNCAT TGTATATCAG TCTTCCCATC AATATTAATT ATTAATATT 1200
TTAGAATTTT TAAATACCAA CTATAAAAAA AAAAAAAA 1239

```

## (2) INFORMATION ON SEQ ID NO. 398:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1663 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

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GAACCTGCTC TCTCTGCTTG TGGTCCCTTG ACGCAGAGAC CGTTCGCTCC CCCACAGCCG 60
TTTGACTGAA GGCTGCTCTG GAGACCTAGA GTAAAAACGGC TGATGGAAGT TGTGGGACCC 120
ACTTCCATTT CCTTCAGTCA TTAGAGGTGG AAGGGAGGGG TCTCCAAGTT TGGAGATTGA 180
GCAGATGAGG CTTGGGATGC CCCCTGCTTT GACTTCAGCC ATGGATGAGG AGTGGGATGG 240
CAGCAAGGTG GCTCCTGTGG CAGTGGAGTT GTTGGCAGAA ACAGTGGCCA GTTGATCGC 300
CTATAAGACA GGGTAAGGTC TGAAGAGCTG AGCCTGTAAT TCTGCTGTAA TAATGATAGT 360
GCTCAAGAAG TGCCCTTGAGT TGGTGTACAG TGCCATGGCC AGCAAGAATC CCAGATTCCA 420
GGTTTTATTA CAAATGTAA GTGTCACTT GCGGATTTTG TAGTACATGC ATGAGTTACC 480
TTTTTCTCT ATGCTGAGA ACTGTCAGAT TAAACAAGA TGSCAAAGAG ATCGTTAGAG 540
TGCACAACAA AATCACTATC CCATTAGACA CATCATCAA AGCTTATTTT TATTCTTGCA 600
CTGGAGAAGT CGTAAGTCAA CTGTTTCTTG ACCATGGCAG TGTTCTGGCT CCAATGGTGA 660
GTGATTCCAA ATAATGGTTC TGTTAACTT TTGGCAGAAA ATGCCAGCTC AGATATTTTG 720
AGATACTAAG GATTATCTTT GGACATGTAC TGCAGCTTCT TGTCTCTGTT TTGGATTACT 780
GGAATACCCA TGGGCCCTCT CAAGAGTGCT GGACTTCTAG GACATTAAAG TATTGTCAG 840
TACATTAAAC TTTTCAATCC CATTATGCAA TCTTGTTTGT AAATGTAAC TCTAAAAAT 900
ATGGTTAATA ACATTCAACC TGTTATTAC AACTTAAAG GAAGTTTCAAT GAATTTGTTT 960

TTATTTTTTA ACAAGATTGG TGAAGTGAAT ATCATGAACC ATGTTTTGAT ACCCCTTTTT1020
CACGTTGTGC CAACGGAATA GGGTGTTTGA TATTTCTTCA TATGTTAAGG AGATGCTTCA1080
AAATGTCAAT TGCTTTAAAC TTAATTTACC TCTCAAGAGA CCAAGGTACA TTTACCTCAT1140
TGTGTATATA ATGTTTAATA TTTGTCAGAG CATTCTCCAG GTTTGCAGT TTTTCTCAT1200
AAAGTATGGG TATTTATGTT CTCAGTTACT CAAATGTTAC TGTATTGTTT ATATTGTTAC1260
CCCAAAATAC ATCGTCTGTA CTTTCTGTTT TCTGTATTGT ATTTGTGCAG GATTCTTTAG1320
GCTTTATCAG TGTAATCTCT GCCTTTTAAG ATATGTACAG AAAATGTCCA TATAAATTTCT1380
CATTGAAGTC GAATGATACT GAGAAGCCTG TAAAGAGGAG AAAAAACAT AAGCTGTGTT1440
TCCCATAAG TTTTTTAA TGTATATTG TATTGTAGT AATATTCCAA AAGATGTA1500
ATAGGAATA GAAGAGTGAT GCTTATGTTA AGTCCTAACA CTACAGTAGA AGAATGGAAG1560
CAGTGCAAT AAATTACATT TTTCCAAAA AAAAAAATA AAAAAAGT1620
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## (2) INFORMATION ON SEQ ID NO. 399:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 2889 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

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GATCAGGCCT GTGGTCCAGC TCACTGCCAT TGAGATTCTA GCTTGGGGCT TAAGAAATAT 60
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AAGGGTGGAA TCGGTGGTGA TCAAAAACCT TAAGAAGACA CCCAACTTTC CAAGTTCTGT 180
TCTCTTCATG AAAGTGTTC TGCCCAAGGA GGAATTGTAC ATGCCCCAC TGGTGATCAA 240
GGTCATCGAC CACAGGCAGT TTGGGCGGAA GCCTGTGCTC GGCCAGTGCA CCATCGAGCG 300
CCTGGACCGC TTTCGCTGTG ACCCTTATGC AGGGAAGAG GACATCGTCC CACAGCTCAA 360
AGCCTCCCTG CTGCTCGCCC CACCATGCCG GGACATCGTT ATCGAAATGG AAGACACCAA 420
ACCATTACTG GCTTCTAAGC TGACAGAAAA GGAGGAAGAA ATCGTGGAAT GGTGGAGTAA 480
ATTGTATGCT TCCTCAGGGG AACATGAAAA ATGCGGACAG TATATTGAGA AAGGCTATTC 540
CAAGCTCAAG ATATATAAAT GTGAAC TAGA AAATGTAGCA GAATTTGAGG GCCTGACAGA 600
CTTCTCAGAT ACGTTCAAGT TGTACCGAGG CAAGTCGGAT GAAAATGAAG ATCCTTCTGT 660
GGTTGGAGAG TTTAAGGGCT CCTTTCGGAT CTACCCCTCTG CCGGATGACC CCACGCGTGC 720
AGCCCCCTCC AGACAGTTTC GGAATTACC TGACAGCGTC CCACAGGAAT GCACGGTTAG 780
GATTTACATT GTTCGAGGCT TAGAGTCCA GCCCAGGAC AACATGGCC TGTGTGACCC 840
TTACATAAAA ATAACACTGG GCAAAAAAGT CATTGAAGAC CGAGATCACT ACATTCCCAA 900
CACCTCAAC CCACTCTTTC GCAGGATGTA CGAACTGAGC TGCTACTTAC CTCAGAAAAA 960
AGACCTGAAA ATTTCTGTCT ATGATTATGA CACCTTTACC CGGGATGAAA AAGTAGGAGA 1020
AACAAATTAT GATCTGGAAG ACCGATTCTT TTCCCGCTTT GGGTCCCACT GCGGCATACC 1080
AGAGGAGTAC TGTGTTTCTG GAGTCAATAC CTGGCGAGAT CAACTGAGAC CAACACAGCT 1140
GCTTCAAAAT GTCGCCAGAT TCAAAGGCTT CCCACAACCC ATCCTTTCCG AAGATGGGAG 1200

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TAGAATCAGA TATGGAGGAC GAGACTACAG CTTGGATGAA TTTGAAGCCA ACAAATCCT1260  
 GCACCAGCAC CTCGGGGCCC CTGAAGAGCG GCTTGCTCTT CACATCCTCA GGACTCAGGG1320  
 GCTGGTCCCT GAGCAGGTGG AAACAAGGAC TTTGCACAGC ACCTTCCAGC CCAACATTTTC1380  
 CCAGGGAAAA CTTCAGATGT GGGTGGATGT TTTCCCCAAG AGTTTGGGGC CACCAGGCCCC1440  
 TCCTTTCAAC ATCACACCCC GGAAAGCCAA GAAATACTAC CTGCGTGTGA TCATCTGGAA1500  
 CACCAAGGAC GTTATCTTGG ACGAGAAAAG CATCACAGGA GAGGAAATGA GTGACATCTA1560  
 CGTCAAAGGC TGGATTCTCT GCAATGAAGA AAACAACAGC AAAACAGATG TCCATTACAG1620  
 ATCTTTGGAT GGTGAAGGGA ATTTTAACGT GCGATTGTGT TTCCCGTTTG ACTACCTTCC1680  
 AGCCGAACAA CTCTGTATCG TTGCGAAAAA AGACGATTTT TGGAGTATTG ACCAAACGG1740  
 ATTTTCAACT CCACCCAGGC TGATCATTCA GATATGGGAC AATGACAAGT TTTCTCTGGA1800  
 TGACTACTTG GGTTCCTTAG AACTTGACTT GCGTCACAGC ATCATTCTGT CAAAATCACC1860  
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 GACAGCCTCC CTCTTTGAGC AGAAGTCCAT GAAAGGATGG TGGCCATGCT ACGCAGAGAA1980  
 AGATGGCGCC CGCGTAATGG CTGGGAAAGT GGAGATGACA TTGGAATATC TCAACGAGAA2040  
 GGAGGCCGAC GAGAGGCCAG CCGGGAAAGG GCGGGACGAA CCCAACATGA ACCCCAAAGCT2100  
 GGACTTACCA AATCGACGAG AAACCTCCTT CCTCTGGTTC ACCAACCCAT GCAAGACCAT2160  
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 CCTGCTGCTC TCGTGGCCGC TGCTCCTCTA CTCTTGGCCG AACTATTGTT CAATGAAGAT2280  
 TGTAAGCCCA AATGTGTAAC AAAGGCAAGG GCTTCATTTC AAGAGTCATC CAGCAATGAG2340  
 AGAATCTCTG CTCTGTAGAC CAACATCCAG TGTGATTTTG TGTCTGAGAC CACACCCAG2400  
 TAGCAGGTTA CGCGCTGTCA CCGAGCCCCA TTGATTCCCA GAGGGTCTTA GTCTCGAAA2460  
 GTCAGGCCAA CAAGCAAGCT TTGCATCATG TTATCTCTTA AGTATTAATA GTTTTATTT2520  
 CTAAAGTTTA AATCATGTGT TTCAAATAT TTTTCAAGGT GGCTGGTTCC ATTTAAAAAT2580  
 CATCTTTTTA TATGTGCTCT CGGTTCTAGA CTTCAAGCTT TGGAAATTGC TAAATAGAAT2640  
 TCAAAATCTC CTGCACTCTG AGGTGATATA CTTCAATATT GTAATCAACT GAAAGAGCTG2700  
 TGCATTATAA AATCAGTTAG AATAGTTAGA ACARTTCTTA TTTATGCCCA CAACCATTTG2760  
 TATATTTTGT ATGGATGTCA TAAAGTCTA TTTAACCTCT GTAATGAAAC TAAATAAAAA2820  
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 GGGGTGTGG 2889

(2) INFORMATION ON SEQ ID NO. 400:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1774 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

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TGAAGGAAGT AACAAAGTG GGAACCCCT GATAACCCC CTCAGGATCC TCATGGAGAA 60
CTTACCTATC CAGGAGAAAT AGCAAAGGGG AAAGAAGCTGG CCCCCCCTG ATTCCGATGA 120
CCCTCCCCCC GGGTCCCCCT CCCACAACAT GTGGGAATTC CCAGAAGATA AATTCAAGTT 180

GCAATTTTCAG TGGGGACATA GCCCACCCCT ATATCACTGG TGATGCCCAC TTCTTCAGTA 240
TTAGGGGATTC TCAGTCAGAA GAGACCCCTT GTGTGGCCTG AGTCCCCTCA GGAGGAAGGT 300
GGACAACAGA GAAATGAGAG TTTTGATATT TTCTGAAGA GGAACATGTG TTAGAGATGA 360
AGAAATCTCC AAGGCTCATG CAGTTGCTTA GAATAATCAT TACTGTTATA TGAGAAACAT 420
TTTAGTAATT TAATAAARGG ATAATGTTTA TTTAAAAAAC CTGACTTTTC CAGAGTAATT 480
TTGTTTTGCA CATTTCATGT TATTGAAGTG GACTAATTTT TATAATGCAA ATCAGAGTTA 540
AATATTAATA ATTGTGTAATA TACAATTGAC ATAGGAATTA CATTAATAATA TTAGGAAGAA 600
ACAAGGACAA ATTTAGACCT TGAATCCGAA GAGATAAAGC TTACTTGACT TTCAAATGGA 660
GAGATGATGA AAACCCACTC ATTCAGTCTT TCAGAACAAA AAGACAGTCA TCTGATAAGA 720
GTATGACATG GATGAAATGC CCTACAGGGG CCTTGGACAT CTTTAATTTT TGCGATTATG 780
TGAAAGAGGT GGACTTTTACA GATAATGGAG CAGAAGCCAA CATTAGTAAA AGGAATCCCA 840
ACTTCTTCCC ATAGAATTAG AATCATGTGA AAGTACAATA AACTTCTTGT TCAAATTACC 900
AGCATCAGAG AGCTTCCCAT TTGCATCTAG ACCTTGAATT TATATTATT GATCAAGTTC 960
TAATTTGTAT GTATATTTTG TGCATATTCA CCAATAACAG TTAATAATTAA TTATGTGTTA1020
TAGTTAATAT ATGCACCTAC CTCTCTCCGT TAGTGATCA GTAAATGTGT TATTTTGTCA1080
TTTTTCCAAA GAGAGTGTGT TAGGTTTTC CTGTAGTTCT TCCTTTATAG CTTTTCTTCT1140
GATAACCATG ACTTCAGGAG CTTTAAACT ATCTATCTTG CATTTGTGTC TGGCGGAGAA1200
CTAGCCATCA GCCTCCTGAA GCCTGCCATC ATTGTTAATT TGAGGACTCG CGTGTCTTGG1260
GGCTCAGAAG GTAAAGAACT ATTTGAGCAG ATGTGTGTGG GTGGCACTGG ATTCACCCCA1320
ACTGCCAAGT TAGTATTGTT AGAGATTTC TTTTACAACA CAAAAATAAG CCTGTGTCAA1380
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ACGAAGACAA GAATCCAAAT GTACTTGGGG ACAAGAATTA GTCCCCAAAT TCAGTGTTC1560
TCCTAGTATT AAACATTGCC CCTTTCGACA AATTTGGAT TTCAACTCTG GTATATTTC1620
GTAACCTGCT TGATTTATTA GGTACTGGG TAGATGACAT TAGAATGTAG ATAGCGTGCA1680
CGCTATGATA GACTCTGCTA AGACATGTC CCAAGTGCCA GCAGCAATGT AGATATGTGT1740
GACAGTGGTC ATGTAGAAGT TATAAGCAG AGTA 1774

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## (2) INFORMATION ON SEQ ID NO. 401:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3982 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

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CCCAAGTGTG ATGCATTGTT CTTCAGATGT TGAAGAAGAAA GCAAAAAATA CTTTCTAACT 60
TAAGACAGAA TTTTAAACAA AATGAGCAGT AAAAGTCACA TGAACCACTC CAAAATCAGT 120
GCATTTTGCA TATTTTAAAA CAAAGACAGC TTGTTGAATA CTGAGAAGAG GAGTGAACAG 180
AGAAGGTCTG TACTAACAAA GCCAAATTCC TCAAGCTCTT ACTGGACTCA GTTCAGAGTG 240
GTGGGCCATT AACCCCAACA TGAATTTTTT CCATATAAAT CTCAATGAAT TCCCTTTTCAT 300

TTGAATAGGC AAACCCAAAT CCATGCAAGT GTTTTAAAGC ACTGTCCTGT CTTAATCTTA 360
CATGCTGAAA GTCTTCATGG TGATATGCAC TATATTCAGT ATACGTATGT TTTCTACTT 420
CTCTTGTAAG ACTGTTGCAT GATCCAACCT CAGCAATGAA TTGTGCCTAG TGGAGAACCT 480
CTATAGATCT TAAAAAATGA ATTATTCTTT AGCAGTGTAT TACTCACATG GGTGCAATCT 540
TTAGCCCCAG GGAGGTCAAT AATGTCTTTT AAAGCCAGAA GTCACATTTT ACCAATATGC 600
ATTTATCATA ATTGTGTGTT AGGCTGTATA TTCAAGCCTG TTGCTCTAAC ATTTTGTATA 660
AAAAAGACAA ACAGAAATTA TCTGTCAATT GAGAAGTGGC TTGACRAATCA TTTGAGCTTT 720
GAAGCAGTCA CTGTGGTGTA ATATGAATGC TGTCTAGTGT GTCATAGTAC CAAGGGCAGC 780
TGTCTCCCTT TGTATAACT GATTTCCCTT TTAGTCTCTT ACTGCTAAAT AAGTTAAATTT 840
TGCAATTTGC AGAAAGAAAC ATTGATTGCT AAATCTTTTT GCTGCTGTGT TTTGGTGTTT 900
TCATGTTTAC TTGTTTTATA TTGACTGTTT TAAGTATGAG AGGCTTATAG TGCCCTCCAT 960
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GAATCTGAGG GAAGATTAT GTTTCGTTTT GGAGGATAGC TCAAGTTGAA TTTCTTTCC2160  
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 TTTATTAGAT AGCCCTGAAT TCACTCTAAT TATAAACAGG GAGTGTAAAC TGCCCCCAGA2280  
 TGTTCCTGGG CTGGGTAAAA GCAGCTGGAG TGAAGCACTC ATTTTCCATA AAGGTAACAA2340  
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 GTCTGTGTAT ACTGAGTTGG AAGTGATTTC AGCACATTCT TTTTGTAGTG AGTGAAAGTT2460  
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 ACTTTATTAA CTATAATATG GTTACAGCTA TTATATAAAT ATATATTCTG GTTATAGTTT3180  
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 GGATGAGTGC TGCCTTGACT ACTGCTATCA GGATTGTGTT GTGTGGAATA TTCATCTACA3780  
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## (2) INFORMATION ON SEQ ID NO. 402:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1876 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

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CTCTTGGATC CCCTGGACCA CTGGGCATAC TCGCCATCCT CTCCCGGAGA TCTGGGCAGT 60
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CACACCTCTG TGCCCACTCT TGAAGCTGTT GGGAAATATT CAGCAATGTC CGCATCAACT 180
TGCAGAAGAA TATAAATGAC ATTTCAAGGA TAGAAGATAC CTGATTTTTT TTCCTTTTAA 240
TTTTCTGTGT GCCAATTTC AAGTTCCAAGT TGCTAATACA GCAACAATTT ATGAATTGAA 300
TTATCTTGGT TGAAAAATAA AAGATCACTT TCTCAGTTTT CATAAGTATT ATGCTCTCTC 360
TGAGCTATTT CATCTATTTT TGGCAGTCTG AATTTTTTAA ACCCATTTAA ATTTTTTTTC 420
TTACCTTTTT ATTTGCATGT GGATCAACCA TCGCTTTATT GGTGAGATA TGAACATATT 480
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CACTGTTTAA GGAGTTAGTG GATTACTGCC ATTCACCTCA TAATCCAGTA GGATCCAGTG 720
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CTTCTTGAAA TTTTAACCTA TGATATTTTC TGTGCTGAA TATTTGTTAT GTAGATAACA 840
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CTCGCTTTAG GTCAGCAGCC TCCTGAAAGA CCAAAATTAG AATATCCATG ACCTAGTTTT 960
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ACGCTTTCC TGAATCCAAAC TAATCCATCA CCGGGGTGCT TTAGTGGCTC AACATTGTGT1260
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CTCTCTTGA TTTTGGCCTC TTCCAGTCTT CCTGACACTT TAATTACCAA CCGTTTACCT1740
ACTTTGACTT TTTGCATTTA AAACAGGACA CGGGGCAGGG AGAAAAGGCT TTTAGTTTTT1800
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1876

## (2) INFORMATION ON SEQ ID NO. 403:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1216 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

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TCTGTTCTGT  GGGAACACTGT  TACTGTTCTT  CCGTGGCCAA  CCATGGCGGC  CACCAGCCCT  60
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CGCCCCACAC  CTCGCTCCCC  CAGTCCCTTC  CCAGCCTGGC  GGTCAGAGAC  TGGCTTGACG  180
CCTCCACGCA  GCCCGGCCAC  CAGGATTTC  ACAGGGTGTA  TGGGCAGCCG  TCCACCAAC  240
ACTACGTGAC  GAGCTAACGC  CACGCAGGCG  GCGGGGCGCT  GGGGAATCTT  CCTCCCCAGC  300
CCCCGGGCTC  GGGAGTTATG  CATCCAGAGA  CCTGCCCTTC  TACCTTCTCT  GCCTCCCCCTC  360
TTECTCATTC  CATGCCCCCA  GGTCTTTTCC  TTTTGGATTT  TGTTTTGGTT  TTGGCTTTGT  420
TTTTGATTTT  TTTTATTAT  GAATCTCCTG  GACGCAGAGG  TGACAGTGGG  AGCTGGCCTG  480
GGCCAGGACG  GCAGGTGGCC  CTGGAGATGG  GAAAGTGTCT  GTGTGAGGCC  GCTGAGCTCT  540
CTCTCTGTTT  CTCCTTTTTT  CCTCTACTCC  TTCCCCCTCA  CACCCCCGTG  GCTGGAAGGA  600
ACCTCGGCTT  CCGTGAAAGC  TTGGGGGTCC  CACCCCTCTT  ACCCCACCCG  GGAGGAACGC  660
CCAGGGCCCC  GGGCTTGTCT  CTCCTCTTGT  TTTCTTTTGT  GGCAGTTTGA  TCACTGATCG  720
AGTAAGGAAT  GACCTTTAGA  TTGTGCGACT  TTTGTTTTTG  TTTTTTAA  TTTTTTAA  780
CCAAGAATGA  TTTCTCCTGC  TTCTCTCTCC  TCACCATCTT  CCCAGACGGA  GTTCAAAGGC  840
CACTTCTCAA  GCAGCTTTTG  GCACCTTCAG  CCTCAGAGTG  GAATCTTTTA  AAGACAGGAC  900
CCCTATGTCC  AGGAAAGGGG  AAAAGGAAC  TTGCCAATGA  TAGTGACCAC  AGCAAAAGCA  960
ATAAAATAT  AAAATAAAAA  ACRAATAGCAC  AGCCCTTGTT  GAGGTCAGCA  GGGAGGAGGG  1020
GCTGCCCGGA  GTTGGGTCTT  TGCCCTGGAT  TTGACACAGC  AACTTCTCTG  AGTGAGCACT  1080
TTGTATGAAT  CGTGGACTTC  CTGTTCTCAA  GCGCAGGTA  TTTATTCTGT  ATCTGTCTAG  1140
AGCACACACC  AAAATCCAAC  CTCTAATAA  ACATGATGGC  GCAGTCCCAA  AAAAAAGAA  1200
CAGAAGAA  AAAGGG

```

1216

## (2) INFORMATION ON SEQ ID NO. 404:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 271 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

RPRAGASIST LAGLSLKEGE DQKEIKIEPA QAVDEVEPLP EDYYTRPVNL TEVTTLQQR 60  
 LQPDFQPVCA SQLYPRHKHL LIKRSRLCRK CEHNLSKPEF NPTSIKFKIQ LVAVNYIPEV120  
 RIMSIPNLRY MKESQVLLTL TNPVENLTHV TLFECEEGDP DOINSTAKVV VPKELVLAG180  
 KDAAAEYDEL AEPQDFQDDP DIIAFRKANK VGIFIKVTPQ REEGEVTVCF KMKHDFKNLA240  
 APIRPIEESD QGTEVIWLTQ HVLSLGLPLL P 271

## (2) INFORMATION ON SEQ ID NO. 405:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 133 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

DLKQDQGGKQK ICIFLKS LGH LLTILLQKTR CSWWSTLSSF ILENIIIEIKV SNPTPGYQVK 60  
 TASLLLGQNC GLLAELFYGL QSKWSYLTHH MTKVLNLVRG KVLNIQFWIQ EIIIVNFPFFK120  
 SMERMLVENI LKI 133



## (2) INFORMATION ON SEQ ID NO. 406:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

RGPGHLLKPN GGPPMKLGYG RNLDISPRLE LNRETVKRSI RFHRFWPLIP NSFPHNSVFL60  
 VSMKCLESHR KPVKIFLKKK KPQKTDHLSI QWTSI 95

## (2) INFORMATION ON SEQ ID NO. 407:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 55 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

YLSLCPCWPG NFFQWCLLEE VFSSCHFKEI KLEIEYGWHD CTLLVLLFFY SSVPL 55

## (2) INFORMATION ON SEQ ID NO. 408:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 127 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

LQEAPCGEHG RHLHKSAMRR DTESELHHQR QVQGAETVGS GQGSAAFSGP SPYARGPGPD 60  
LPLLGGQHLS IRRWFKCVTM SQCVLELPFS NANLPSLHIS PHPWTRFCVS ESGNLLKRGGL20  
STPGLLV 127

(2) INFORMATION ON SEQ ID NO. 409:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

KGVGLLIMGG QGQVLGHRER VRRMLQTPAH CPRSPLPAPA SDGAALIPCL SSLQIYEGAY60  
HVLHKELPEV TNSVFHEINM WVSQRTATAG TASPF 95

(2) INFORMATION ON SEQ ID NO. 410:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 296 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

VVLAPTFGH YVCTVISHAH EVRQMQLERR VRSGVMSEKD HMVIMHDVLD AQWLYDNHKD 60  
ESYLRRVVP LEKLLTSHKR LVMKDSAVNA ICYGAKIMLP GVLAYEDGIE VNQEIVVITT120  
KGEAICMAIA LMTTAVISTC DHGIVAKIKR VIMERDTYPR KWGLGPKASQ KKLMIKQGLL180  
DKHGKPTDST PATWKQEVD YSESAKKEVV AEVVKAPQVV AEAATAKGS ESESESDET240  
PPAAPQLIKK EKKKSKKDKK AKAGLESAGAE PGDGDSDTTK KKKKKKKAKE VELVSE 296

## (2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 280 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

RQGGGSLRS FPLRWLGRHD AVQGNMADAE VIILPKKHKK KKERKSLPEE DVAEIQHAE 60  
 FFIKPEKVA KLDTSQWELL LKNFDKLNVR THTYTPLACG SNPLKREIGD YIRTGFINDL120  
 KPSNPSSEHV VAWIRAILRV EKTGHSGTLD PKVTGCLIVC IERATRLVKS QQSAGKEYVGI180  
 IVRLHNAIEG GTQLSRALET LTGALFQRFP LIAAVKRQLR VRTIYESKMI EYDPERRLGI240  
 FWVSCEAGTY IRTLGVHSDQ SRARGTSDAG ASEGFSWSHE 280

## (2) INFORMATION ON SEQ ID NO. 412:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 360 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

RHPHPEGVMG FSRGCGSASS ILWKPDHCFW QRFPGHQEFE EERLRPAGMH GTQRGRGGQV 60  
 DPAAHCPGAH GETHLPDPQ REDHGHGGAT TFSLNCSAAG TPTPSLVWVL PNGTDLQSGQ120  
 QLQRFYHKAD GMLHISGLSS VDAGAYRCVA RNAAGHTERL VSLKVGLKPE ANKQYHNLS180  
 IINGETLKLFP CTPPGAGQGR FSWLTPNGMH LEGPQTLGRV SLLDNGTLTV REASVFDRT240  
 YVCRMETEGY PSVTSIPVIV IAYPPRITSE PTFVIYTRPG NTVKLNCMAM GIPKADITWE300  
 LPDKSHLKGAG VQARLYGNRF LHPQGSLLTQ HATQRDAGFY KCMARNILGS DSKTTYIRVF360

## (2) INFORMATION ON SEQ ID NO. 413:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 314 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

```

EEGDYTCFAE  NQVGKDEMRV  RVKVVVTAPAT  IRNKTYLAVQ  VPYGDVVVTA  CEAKGEPMKP  60
VTWLSPTNKV  IPTSSEKYQI  YQDGTLLIQK  AQRSDSGNYT  CLVRNSAGED  RKTVVIHVNV  120
QPPKINGNPN  PITTVREIPA  GGSRLKLECK  AEGIPTPRVL  WAFPEGVVLP  APYYGNRITV  180
HGNGSLDIRS  LRKSDSVQLV  CMARNEGGEA  RLILQLTVLE  PMEKPIFHDP  ISEKITAMAG  240
PQHSASTALP  RGP RHPAWCG  SFPMAPICRV  DSSCSASTTR  LTACYTLAVS  PRWTLGP TAA  300
WPAMPLATRR  GWSP

```

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## (2) INFORMATION ON SEQ ID NO. 414:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 109 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

```

RPVPAKLNPR  SWPRTAGALP  LRPPPLTMAV  FHDEVEIEDF  QYDEDESETYF  YPCPCGDNFS  60
ITKEDLENGE  DVATCPSCSL  IIKVIYDKDQ  FVCGETVPAP  SANKELVKC

```

109

## (2) INFORMATION ON SEQ ID NO. 415:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

YAKSTATSHG NLTLTPTWNA ISLALSKHKQ KLRYNITCS DLAKSFKHST YYTGMLCSSH 60  
SVTNFTSFGC FSPHLVLTSK EYAEYKKSPP SFITSFWTF L VH 103

(2) INFORMATION ON SEQ ID NO. 416:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 144 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

YTMKIIYFTR KILYXQGGIL KYNTPGXSFL LYIMIVSFHI SWXLXGKGT XKSIFIYIKT 60  
KCKXQRLXPP KCLVSLNNM NEXKMNQIT WXTHRRXNKK AQEIKSCFKL GHIKGGKGS120  
RRVRKISSQA TKNLXRRQPP NXIR 144

(2) INFORMATION ON SEQ ID NO. 417:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 74 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

LILMGRLIYN XNYLFYKXDS IHXGRHLEVQ YTRXFISSLH YDCEFPYKLX TXHXKGNXKI60  
 HFYIHKNKTX PXET 74

## (2) INFORMATION ON SEQ ID NO. 418:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 121 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

YFFFTLCQRN RVFDISSYVK EMLQNVNCFK LKLPKRPRY IYLVYIMFN ICQSILQVCS 60  
 FISIKYGYV AQLLKWYCIY YICTPNNIVC TFCFLYCICA GFFRLYQCNL CLLRVVQKMS120  
 I 121

## (2) INFORMATION ON SEQ ID NO. 419:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 114 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

FFFFFFFFS FQRIHFFFFFF FFFFEKGNVI YLHCFHSSTV VLGLNISITL LFPIYILLEY 60  
 YYKYNIQFKK TYGETQLMEF SPLYRLLSII RLQWKFIWTF SVHILKGRDY TDKA 114

## (2) INFORMATION ON SEQ ID NO. 420:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 765 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

```
IRPVVQLTAI EILAWGLRNM KNFQMASITS PSLVVECGGE RVESVVIKNL KKTNPFPSSV 60
LFMKVFLPKE ELYMPPLVIK VIDHRQFGRK PVVGQCTIER LDRFRCDPYA GKEDIVPQLK120
ASLLSAPPCR DIVIEMEDTK PLLASKLTEK EEEVDWWSK FDASSGEHEK CGQYIQKGYS180
KLKIYNCELE NVAEFGELTD FSDTFKLYRG KSDENEDPSV VGEFKGSFRI YPLPDDPSVP240
APPRQFRELP DSVPQECTVR IYIVRGLQLQ PQDNNGLCDP YIKITLGGKV IEDRHHYIPN300
TLNBPVFGMY ELSCYLPQEK DLKISVYDYO TFRDEKVGE TIIDLENRFL SREGSHCGIP360
EEYCVSGVNT WRDQLRPTQL LQNVARFKGF PQPILSEDSG RIRYGGRDYS LDEFEANKIL420
HQHLGAPPEER LALHILRTQG LPVEHVETRT LHSTFQPNIS QGKLQMWVDV FPKSLGPPGP480
PFNITPRKAK KYLLRVIIWN TKDVILOEKS ITGEEMSDIY VKGWIPGNEE NKQKTDVHYR540
SLDGGGNNFN RVVFPPDYLP AEQLCIVAKK EHFWSIDQTE FRIPPRLIQ IWNDKDFSLD600
DYLGFLELDL RHTIIPAKSP EKCRLDMIPD LKAMNPLKAK TASLFEQKSM KGWWPCYAEK660
DGARVMAGKV EMTLEILNEK EADERPAGKG RDEPNMNPKL DLPNRPETSF LWFTNPFCKTM720
KFIVWRFRKW VIIGLLLELI LLEFVAVLLY SLPNYSMKI VKPNV 765
```

## (2) INFORMATION ON SEQ ID NO. 421:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 289 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

```
ETQVVIQRKL VIVPYLNDQP GWDSKFRLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60
FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVLGFFG120
CDVERRAWWP QTLGSEIHHP LKFSGLNVGL EGAVQSPCFH VLRDQLSPFE DVKSKPLFRG180
PEVLVQDFVG FFFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISPGIDSR240
NTVLLWYAAV GKAGKESVF QINNCFSYFF IPGKGVIID RNQVQFFLR 289
```

## (2) INFORMATION ON SEQ ID NO. 422:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 90 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

FFLYSFSSDN HDFSFKTIY LAFVSGGELA ISLLKPAIIV NLRTGLSWGSG EGKELFEQMC60  
 VGGTGFHPTA KLVLEISFY NTKISLCQRF 90

## (2) INFORMATION ON SEQ ID NO. 423:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

TPSGSSSWRTY LSRNSKGER TGPPLIPMTL PPGPLPTTCG NSQKINSSCN FSGDIAQTHI60  
 TGDHFFSIR DSQEETPCV A 81

## (2) INFORMATION ON SEQ ID NO. 424:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes



- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

ENWASRYFQS SFTEQKVWVG HWLEGDSPTL TVTIWAATGG IVQLASRCIP HLKVCWIKAI 60  
YTLAKSKAKE IALDPESQQD HLIFPNQHLG QQLPSTFLFH SWFFFFFELQ DLAVTQDGVQ120  
WHDHGSLLQP 129

(2) INFORMATION ON SEQ ID NO. 425:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 122 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

EAQKWDCIWT KNYKKVQSLV SRMQALALGD GSSLENPAAD SLFQRRSFER RVCYISFFTV 60  
TLWRLKDLVV SCFLKITGIW RPKPFWTDI SSKYFFIKVF EGDDFLDLWL DILGFDPYIV120  
LS 122

(2) INFORMATION ON SEQ ID NO. 426:

- (i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 105 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

REFKSPQRQN HNMSRRNKKL LDIPGSFLYD SGLQVKFSL SSEEFELIPA KYFNLFITAS 60  
SPIFFLGKGM LGLGPKLLAG GGAMCHSITD GCKCFTEQGS GLQQ 105

## (2) INFORMATION ON SEQ ID NO. 427:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 96 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

EKYEELRRKK KKKKRTNNLN CLLQNVG:FM LREEFQGMAM ECTSMWADFQ QTLFPLFKEL60  
VDYCHSLHNP VGSSDPYKLE NIIFCLLMIQ LMPYSS 96

## (2) INFORMATION ON SEQ ID NO. 428:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 151 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

RKKGETEREL SASTQTLSHL QGHLPSWPRP APTVTSASRR FIIKKNQKQS QNQNKIQKEK 60  
TWNGMRKRG GEEGRAGLW MHNSRARGLG RKIPQRPAAC VALARHVVEG GRLEIHPVEI120  
LVAGLLGGVK PVSQRQAGKG LGDGGCGRER V 151

## (2) INFORMATION ON SEQ ID NO. 429:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 150 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

```
RHAGGGALGN LPPQPPGSGV MHPETCPSTF LASPLPHSIA PGLFLDFFVL VLALFLIFFY 60
YESPGRRGDS GSWPGPGRQV ALEMKGKLCR GAELSLCFSF FPLLLPLHTP VAGRNLGFPPE120
SLGVPPFLPH PGCTPRAPGL FLLLSFWAV                               150
```

(2) INFORMATION ON SEQ ID NO. 430:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 285 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

```
SWRTGGWAYA GDRLNKTSV SVASWASSLN ARMDNRFATA FVIACVLSLI STIYMAASIG 60
TDFWYEYRSP VQENSSDLNK SIWDEFISDE ADEKTYNDAL FRYNGTVGLW RRCITIPKNM120
HWYSPPERTE SFDVVTCKVS FTLTEQFMEX FVDPGNHNSG IDLLRITYLWR CQFLLPFVSL180
GLMCFGALIG LCACICRSly PTIATGILHL LAGLCTLGSV SCYVAGIELL HQKLELPDNV240
SGEFGWSFCL ACVSAPLQFM ASALFIWAAH TNRKEYTLMK AYRVA                285
```

(2) INFORMATION ON SEQ ID NO. 431:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 116 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

LCPEFWAIPM HVFGYGDTPS PQSHCAIVSK KCIILSLFIC LITNEFIPDA FIQITGIFLN 60  
WTSIFIPEVC ANGGCHVDGG NEAKHTSNYK CCSKTVIHSG IQTARPGCYG DRGLVL 116

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## Claims

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID Nos. 21, 24-27, 29-40, 43, 44, 46-48, 50-63, 65, 67, 69, 72, 73, 75, 77-80, 82, 83, 85-86, 88, 90, 92-127, 391-403,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-127 and 391-403, or a complementary or allelic variant thereof.

3. Nucleic acid sequences Seq. ID Nos. 1-127 and 391-403, characterized in that they are expressed elevated in normal bladder tissue.

4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-127 and 391-403 for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has % homology to a human nucleic acid sequence.

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a

sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is *E. coli*, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 1-127 and 391-403, which can be obtained according to claim 19.

21. An antibody according to claim , wherein it is monoclonal.

22. An antibody according to claim , wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.

27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 128-390 and 404-431 as tools for finding active ingredients against the bladder tumor.

28. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-127 and 391-403 for expression of polypeptides that can be used as tools for finding active ingredients against the bladder tumor.

29. Use of nucleic acid sequences Seq. ID Nos. 1-127 and 391-403 in sense or antisense form.

30. Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 as pharmaceutical agents in gene therapy for treatment of the bladder tumor.

31. Use of polypeptide partial sequences Seq. ID Nos. 128-390 and 404-431 for the production of a pharmaceutical agent for treatment of the bladder tumor.

32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 128-390 and 404-431.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

34. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-127 and 391-403.



36. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

37. Use according to claim 36, wherein the regulatory element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

**Abstract**

Human nucleic acid sequences -- mRNA, cDNA, genomic sequences -- from normal bladder tissue, which code for gene products or portions thereof, and their use, are described.

In addition, the polypeptides that can be obtained by way of the sequences and their use are described.

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# Systematic Gene Search in the Incyte LifeSeq Database

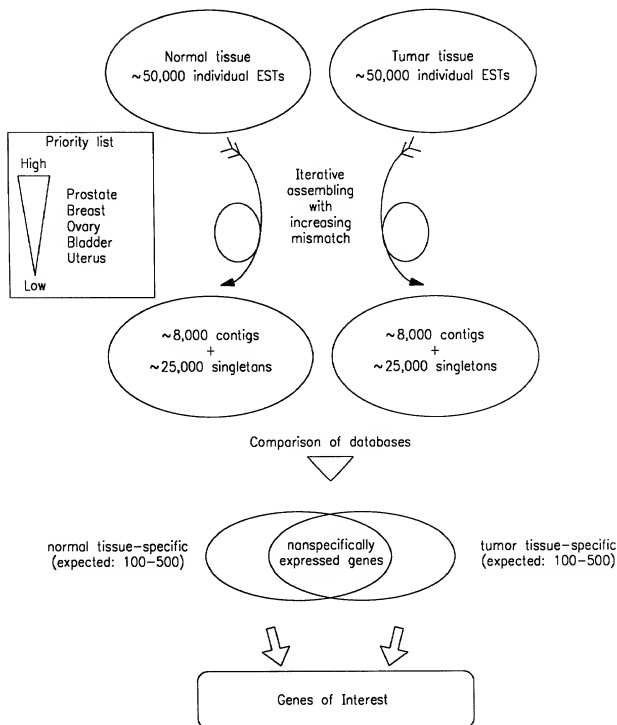
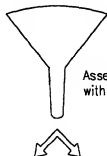


FIG. 1

# Principle of EST Assembly

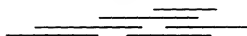
~50,000 ESTs per tissue



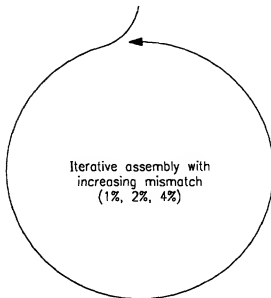
Assembly at 0% mismatch  
with GAP4 (Staden)

Contigs

Singletons



Contigs increasing in  
number and length



Iterative assembly with  
increasing mismatch  
(1%, 2%, 4%)

5000-6000 Contigs    ~25,000 other singletons



~30,000 consensus-  
sequences per tissue

FIG. 2a

~50,000 ESTs  
of a tissue  
(e.g.: uterus tumor)

GAP4 Assembly 1st Round:  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 0

GAP4-Database 1:  
Contigs 1 Singletons 1

unassembled  
ESTs

GAP4 Assembly 2nd Round:  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 1

GAP4-Database 2:  
Contigs 2 Singletons 2

unassembled  
ESTs

GAP4 Assembly 3rd Round:  
minimum initial match: 20  
maximum pads per read: 8  
maximum percent mismatch: 2

GAP4-Database 3:  
Contigs 3 Singletons 3

unassembled  
ESTs

FIG. 2b-I

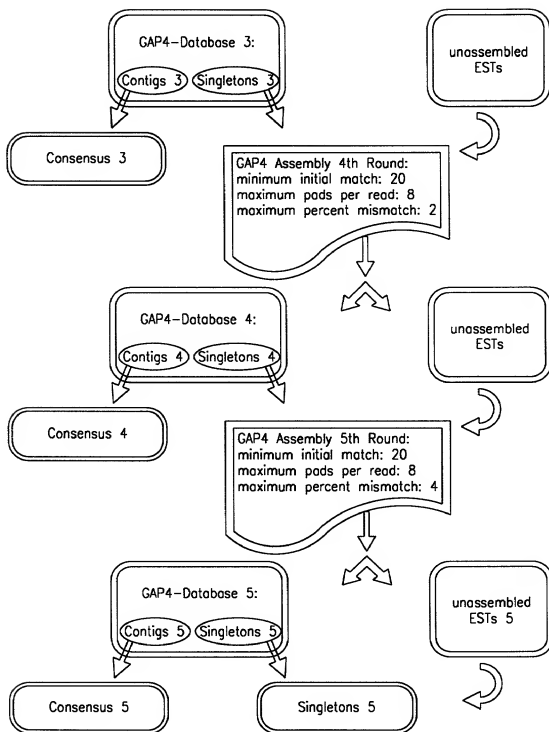


FIG. 2b-2

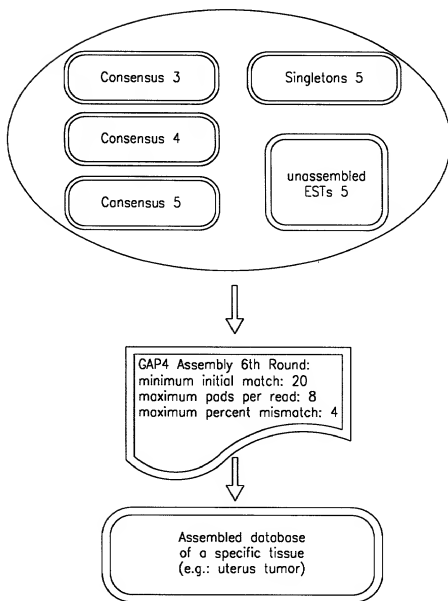


FIG. 2b-3

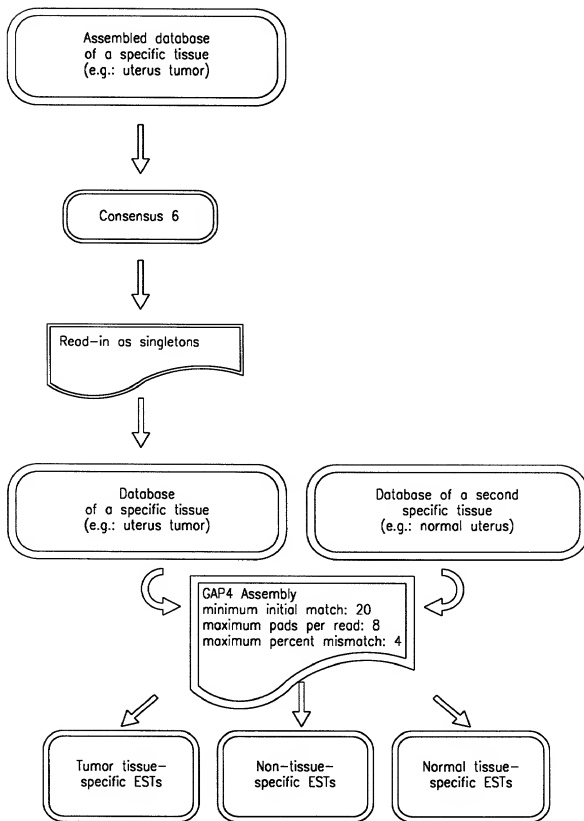


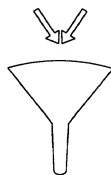
FIG. 2b-4



In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
cancer tissue



Assembly at 4% mismatch

Normal tissue  
Specific genes

Cancer tissue  
Specific genes

Genes expressed in both tissues

**FIG. 3**

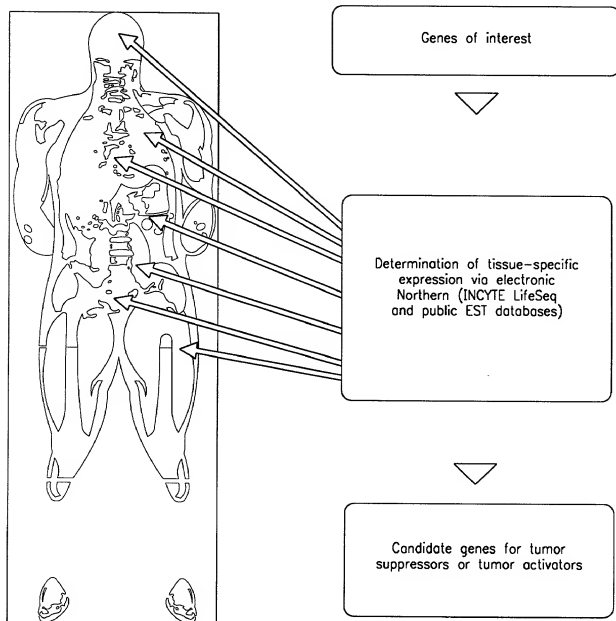


FIG. 4a

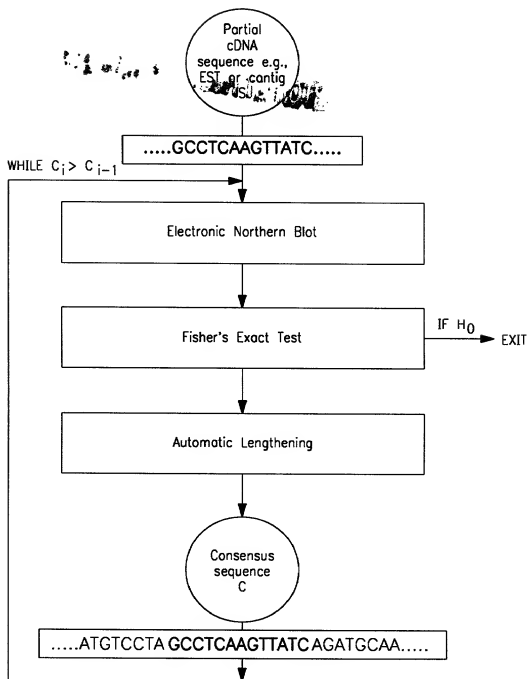


FIG. 4b

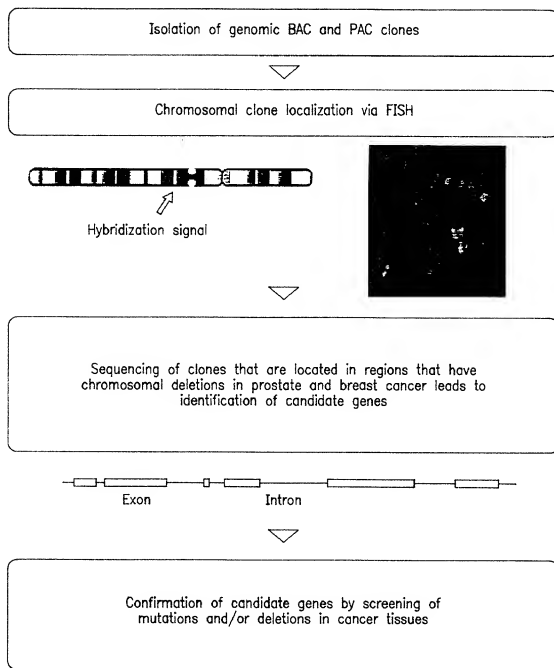


FIG. 5

Attorney Docket Number: SCH 1781**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE**

the specification of which

☐ is attached hereto

☒ was filed on 15 April 1999 as United States Application Number or PCT International Application Number PCT/DE99/01163 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56.

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT international application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT international application having a filing date before that of this application on which priority is claimed.

| PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119 |         |                      |                  |
|--|---------|----------------------|------------------|
| APPLICATION NO.  | COUNTRY | DAY/MONTH/YEAR FILED | PRIORITY CLAIMED |
| 198 18 620.7   | Germany | 21 April 1998        | X                |
|  |         |                      |                  |

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

| PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e) |             |
|--|-------------|
| APPLICATION NUMBER                                 | FILING DATE |
|  |             |

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT international application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT international application in the manner provided by the first paragraph of 35 U.S.C. §112.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application.

| PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120 |             |                                       |
|---|-------------|---------------------------------------|
| APPLICATION NO.   | FILING DATE | STATUS — PATENTED, PENDING, ABANDONED |
|   |             |                                       |

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544); John L. White (17,746); Anthony J. Zeiano (27,969); Alan E.J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brion P. Heaney (32,542); Richard J. Taverro (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Nancy J. Axelrod (44,014); James E. Ruland (40,921) and Jennifer J. Branigan (37,432).

Declaration for Patent Application (Continued)

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**FAX (703) 243-6410**

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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**Thomas SPECHT**

Signature

Date

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**Edgar DAHL**

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51587AWO MAXX24-P

Attorney Docket Number: SCH 1781**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

**HUMAN NUCLEIC ACID SEQUENCES OF NORMAL BLADDER TISSUE**

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**PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)**

| APPLICATION NUMBER | FILING DATE |
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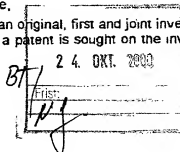
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## Declaration for Patent Application (Continued)

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